

SEQUENCE LISTING

<110> Renner, Wolfgang A.
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 Tissot, Alain
 Maurer, Patrick
 Lechner, Franziska
 Sebbel, Peter
 Plossek, Christine
 Ortman, Rainer
 Luond, Rainer
 Staufenbiel, Matthias
 Frey, Peter

<120> Molecular Antigen Array

<130> 1700.0190005

<140> (To be assigned)

<141> 2002-01-18

<150> US 60/262,379

<151> 2001-01-19

<150> US 60/288,549

<151> 2001-05-04

<150> US 60/326,998

<151> 2001-10-05

<150> US 60/331,045

<151> 2001-11-07

<160> 350

<170> PatentIn Ver. 2.1

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44

1050508.011802

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10050390-011002

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<223> Description of Artificial Sequence: Primer

<400> 10

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<223> Description of Artificial Sequence: Primer

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<210> 12

<211> 33

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<210> 13

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1050888.011802

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<400> 13
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<400> 14
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1 5 10 15
Thr Val Ala Gln Ala
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<210> 15
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Asp Glu Lys Ser Ala Leu Gln Thr Glu Ile Ala Asn Leu Leu Lys Glu
20 25 30
Lys Glu Lys Leu Glu Phe Ile Leu Ala Ala His Gly Gly Cys
35 40 45

<210> 16
<211> 6
<212> PRT
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<223> Description of Artificial Sequence: peptide linker

<400> 16
Ala Ala Ala Ser Gly Gly
1 5

<210> 17
<211> 6
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10050303-0114302

<223> Description of Artificial Sequence: peptide linker

<400> 17

Gly Gly Ser Ala Ala Ala
1 5

<210> 18

<211> 256

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Fos fusion construct

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ctgaccgaca cctgcaggc ggaaccgcac caggtggaag acgaaaaatc cgcgctgcaa 180
accgaaatcg cgaacctgct gaaagaaaaa gaaaagctgg agttcatcct ggcggcacac 240
ggtggttgct aagctt 256

<210> 19

<211> 52

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<213> Artificial Sequence

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<223> Description of Artificial Sequence: Fos fusion construct

<400> 19

Ala Ala Ala Ser Gly Gly Cys Gly Gly Leu Thr Asp Thr Leu Gln Ala
5 10 15

Glu Thr Asp Gln Val Glu Asp Glu Lys Ser Ala Leu Gln Thr Glu Ile
20 25 30

Ala Asn Leu Leu Lys Glu Lys Glu Lys Leu Glu Phe Ile Leu Ala Ala
35 40 45

His Gly Gly Cys
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<210> 20

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<212> DNA

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<221> CDS

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1 5 10

1005000-010000

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Ala Leu Ala Gly Phe Ala Thr Val Ala Gln Ala Cys Gly Gly Leu Thr
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gac acc ctg cag gcg gaa acc gac cag gtg gaa gac gaa aaa tcc gcg 147
Asp Thr Leu Gln Ala Glu Thr Asp Gln Val Glu Asp Glu Lys Ser Ala
      30                35                40

ctg caa acc gaa atc gcg aac ctg ctg aaa gaa aaa gaa aag ctg gag 195
Leu Gln Thr Glu Ile Ala Asn Leu Leu Lys Glu Lys Glu Lys Leu Glu
      45                50                55

ttc atc ctg gcg gca cac ggt ggt tgc ggt ggt tct gcg gcc gct 240
Phe Ile Leu Ala Ala His Gly Gly Cys Gly Gly Ser Ala Ala Ala
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gggtgtgggg atatcaagct t 261

<210> 21
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<213> Artificial Sequence

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      construct

<400> 21
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Thr Val Ala Gln Ala Cys Gly Gly Leu Thr Asp Thr Leu Gln Ala Glu
      20                25                30

Thr Asp Gln Val Glu Asp Glu Lys Ser Ala Leu Gln Thr Glu Ile Ala
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Asn Leu Leu Lys Glu Lys Glu Lys Leu Glu Phe Ile Leu Ala Ala His
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<223> Description of Artificial Sequence: Fos fusion
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      Ala Ala Ala Ser Gly Gly Cys
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1050303.011002

ggt ggt ctg acc gac acc ctg cag gcg gaa acc gac cag gtg gaa gac 102
Gly Gly Leu Thr Asp Thr Leu Gln Ala Glu Thr Asp Gln Val Glu Asp
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gaa aaa tcc gcg ctg caa acc gaa atc gcg aac ctg ctg aaa gaa aaa 150
Glu Lys Ser Ala Leu Gln Thr Glu Ile Ala Asn Leu Leu Lys Glu Lys
25 30 35

gaa aag ctg gag ttc atc ctg gcg gca cac ggt ggt tgc taagctt 196
Glu Lys Leu Glu Phe Ile Leu Ala Ala His Gly Gly Cys
40 45 50

<210> 23
<211> 52
<212> PRT
<213> Artificial Sequence

<220>
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construct

<400> 23
Ala Ala Ala Ser Gly Gly Cys Gly Gly Leu Thr Asp Thr Leu Gln Ala
1 5 10 15
Glu Thr Asp Gln Val Glu Asp Glu Lys Ser Ala Leu Gln Thr Glu Ile
20 25 30
Ala Asn Leu Leu Lys Glu Lys Glu Lys Leu Glu Phe Ile Leu Ala Ala
35 40 45
His Gly Gly Cys
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<210> 24
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<212> DNA
<213> Artificial Sequence

<220>
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construct

<400> 24
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accgaccagg tggaagacga aaaatccgcg ctgcaaaccg aaatcgcgaa cctgctgaaa 120
gaaaaagaaa agctggagtt catcctggcg gcacacgggtg gttgcgggtg tctgcgggcc 180
gctgggtgtg gggatatcaa gctt 204

<210> 25
<211> 56
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Fos fusion
construct

1050598-01302

<400> 25
 Lys Thr Met Ala Cys Gly Gly Leu Thr Asp Thr Leu Gln Ala Glu Thr
 1 5 10 15
 Asp Gln Val Glu Asp Glu Lys Ser Ala Leu Gln Thr Glu Ile Ala Asn
 20 25 30
 Leu Leu Lys Glu Lys Glu Lys Leu Glu Phe Ile Leu Ala Ala His Gly
 35 40 45
 Gly Cys Gly Gly Ser Ala Ala Ala
 50 55

<210> 26
 <211> 26
 <212> PRT
 <213> Homo sapiens

<400> 26
 Met Ala Thr Gly Ser Arg Thr Ser Leu Leu Leu Ala Phe Gly Leu Leu
 1 5 10 15
 Cys Leu Pro Trp Leu Gln Glu Gly Ser Ala
 20 25

<210> 27
 <211> 262
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Fos fusion
 construct

<400> 27
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 tgctgtccct gggttcaaga gggcagcgcgt ggggtgtggg cggcgcgttc tgggtgtgtc 120
 ggtgtgtcga ccgacaccct gcaggcggaa accgaccagg tgggaagacga aaaatccgcg 180
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<210> 28
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 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Fos fusion
 construct

<400> 28
 Ala Ala Ala Ser Gly Gly Cys Gly Gly Leu Thr Asp Thr Leu Gln Ala
 5 10 15
 Glu Thr Asp Gln Val Glu Asp Glu Lys Ser Ala Leu Gln Thr Glu Ile
 20 25 30
 Ala Asn Leu Leu Lys Glu Lys Glu Lys Leu Glu Phe Ile Leu Ala Ala
 35 40 45
 His Gly Gly Cys
 50

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<210> 29
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<220>
<223> Description of Artificial Sequence: Fos fusion
construct

<220>
<221> CDS
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ctg ctc tgc ctg ccc tgg ctt caa gag ggc agc gct tgc ggt ggt ctg 96
Leu Leu Cys Leu Pro Trp Leu Gln Glu Gly Ser Ala Cys Gly Gly Leu
15 20 25 30
acc gac acc ctg cag gcg gaa acc gac cag gtg gaa gac gaa aaa tcc 144
Thr Asp Thr Leu Gln Ala Glu Thr Asp Gln Val Glu Asp Glu Lys Ser
35 40 45
gcg ctg caa acc gaa atc gcg aac ctg ctg aaa gaa aaa gaa aag ctg 192
Ala Leu Gln Thr Glu Ile Ala Asn Leu Leu Lys Glu Lys Glu Lys Leu
50 55 60
gag ttc atc ctg gcg gca cac ggt ggt tgc ggt ggt tct gcg gcc gct 240
Glu Phe Ile Leu Ala Ala His Gly Gly Cys Gly Gly Ser Ala Ala Ala
65 70 75
gggtgtggga ggcctaagct t 261

<210> 30
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<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Fos fusion
construct

<400> 30
Met Ala Thr Gly Ser Arg Thr Ser Leu Leu Leu Ala Phe Gly Leu Leu
1 5 10 15
Cys Leu Pro Trp Leu Gln Glu Gly Ser Ala Cys Gly Gly Leu Thr Asp
20 25 30
Thr Leu Gln Ala Glu Thr Asp Gln Val Glu Asp Glu Lys Ser Ala Leu
35 40 45
Gln Thr Glu Ile Ala Asn Leu Leu Lys Glu Lys Glu Lys Leu Glu Phe
50 55 60
Ile Leu Ala Ala His Gly Gly Cys Gly Gly Ser Ala Ala Ala

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70

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<210> 31
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<212> DNA
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<223> Description of Artificial Sequence: Primer

<400> 31
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<210> 32
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<223> Description of Artificial Sequence: Primer

<400> 32
ggtgggaatt caggaggtaa aaagatatcg ggtgtggggc ggcc 44

<210> 33
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<223> Description of Artificial Sequence: Primer

<400> 33
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<210> 34
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<223> Description of Artificial Sequence: Primer

<400> 34
gcttgcggtg gtctgacc 18

<210> 35
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<212> DNA
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<400> 35
ccaccaagct tagcaaccac cgtgtgc 27

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<210> 36
 <211> 54
 <212> DNA
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 <220>
 <223> Description of Artificial Sequence: Primer

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 <210> 37
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 <400> 37
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 <210> 38
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 <223> Description of Artificial Sequence: Primer

 <400> 38
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 <210> 39
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 <210> 40
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 <400> 40
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 <210> 41
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<212> DNA
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<400> 41
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<400> 42
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<210> 43
<211> 402
<212> DNA
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<223> Description of Artificial Sequence: Modified bee
venom phospholipase A2

<220>
<221> CDS
<222> (1)..(402)

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ile ile tyr pro gly thr leu trp cys gly his gly asn lys ser ser
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ggt ccg aac gaa ctc ggc cgc ttt aaa cac acc gac gca tgc tgt cgc 96
gly pro asn glu leu gly arg phe lys his thr asp ala cys cys arg
20 25 30
acc cag gac atg tgt ccg gac gtc atg tct gct ggt gaa tct aaa cac 144
thr gln asp met cys pro asp val met ser ala gly glu ser lys his
35 40 45
ggg tta act aac acc gct tct cac acg cgt ctc agc tgc gac tgc gac 192
gly leu thr asn thr ala ser his thr arg leu ser cys asp cys asp
50 55 60
gac aaa ttc tac gac tgc ctt aag aac tcc gcc gat acc atc tct tct 240
asp lys phe tyr asp cys leu lys asn ser ala asp thr ile ser ser
65 70 75 80
tac ttc gtt ggt aaa atg tat ttc aac ctg atc gat acc aaa tgt tac 288
tyr phe val gly lys met tyr phe asn leu ile asp thr lys cys tyr
85 90 95
aaa ctg gaa cac ccg gta acc ggc tgc ggc gaa cgt acc gaa ggt cgc 336
lys leu glu his pro val thr gly cys gly glu arg thr glu gly arg
100 105 110

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tgc ctg cac tac acc gtt gac aaa tct aaa ccg aaa gtt tac cag tgg 384
Cys Leu His Tyr Thr Val Asp Lys Ser Lys Pro Lys Val Tyr Gln Trp
115 120 125

ttc gac ctg cgc aaa tac 402
Phe Asp Leu Arg Lys Tyr
130

<210> 44
<211> 134
<212> PRT
<213> Artificial Sequence

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<223> Description of Artificial Sequence: Modified bee
venom phospholipase A2

<400> 44
Ile Ile Tyr Pro Gly Thr Leu Trp Cys Gly His Gly Asn Lys Ser Ser
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Gly Pro Asn Glu Leu Gly Arg Phe Lys His Thr Asp Ala Cys Cys Arg
20 25 30
Thr Gln Asp Met Cys Pro Asp Val Met Ser Ala Gly Glu Ser Lys His
35 40 45
Gly Leu Thr Asn Thr Ala Ser His Thr Arg Leu Ser Cys Asp Cys Asp
50 55 60
Asp Lys Phe Tyr Asp Cys Leu Lys Asn Ser Ala Asp Thr Ile Ser Ser
65 70 75 80
Tyr Phe Val Gly Lys Met Tyr Phe Asn Leu Ile Asp Thr Lys Cys Tyr
85 90 95
Lys Leu Glu His Pro Val Thr Gly Cys Gly Glu Arg Thr Glu Gly Arg
100 105 110
Cys Leu His Tyr Thr Val Asp Lys Ser Lys Pro Lys Val Tyr Gln Trp
115 120 125
Phe Asp Leu Arg Lys Tyr
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<210> 45
<211> 19
<212> DNA
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<220>
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<400> 45
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<210> 46
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<212> DNA
 <213> Artificial Sequence

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 <400> 46
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 <210> 47
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 <212> DNA
 <213> Artificial Sequence

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 <400> 47
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 <210> 48
 <211> 19
 <212> DNA
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 <223> Description of Artificial Sequence: Primer

 <400> 48
 ttagtatttg cgcaggtcg 19

 <210> 49
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 <212> DNA
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 <220>
 <223> Description of Artificial Sequence: Primer

 <400> 49
 ccggctccat cgggtcag 18

 <210> 50
 <211> 36
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 <223> Description of Artificial Sequence: Primer

 <400> 50
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 <210> 51
 <211> 35
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<220>
 <223> Description of Artificial Sequence: Primer

 <400> 51
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 <223> Description of Artificial Sequence: Primer

 <400> 52
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 <220>
 <223> Description of Artificial Sequence: Primer

 <400> 53
 actagtctag aatgagagtg aaggagaaat atc 33

 <210> 54
 <211> 42
 <212> DNA
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 <220>
 <223> Description of Artificial Sequence: Primer

 <400> 54
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 <210> 55
 <211> 51
 <212> DNA
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 <220>
 <223> Description of Artificial Sequence: Primer

 <400> 55
 gtagcaccac ccaaggcaaa gctgaaagct acccagctcg agaaactggc a 51

 <210> 56
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 <220>
 <223> Description of Artificial Sequence: Primer

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<400> 56
caaagctcct attccactg ccagttttctc gagctgggta gctttcag 48

<210> 57
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 57
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<210> 58
<211> 37
<212> DNA
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<220>
<223> Description of Artificial Sequence: Primer

<400> 58
gatgctgggc ccttaaccgc aaccaccgtg tgccgcc 37

<210> 59
<211> 46
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: JUN amino acid
sequence

<400> 59
Cys Gly Gly Arg Ile Ala Arg Leu Glu Glu Lys Val Lys Thr Leu Lys
1 5 10 15
Ala Gln Asn Ser Glu Leu Ala Ser Thr Ala Asn Met Leu Arg Glu Gln
20 25 30
Val Ala Gln Leu Lys Gln Lys Val Met Asn His Val Gly Cys
35 40 45

<210> 60
<211> 46
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: FOS amino
acid sequence

<400> 60
Cys Gly Gly Leu Thr Asp Thr Leu Gln Ala Glu Thr Asp Gln Val Glu
1 5 10 15
Asp Glu Lys Ser Ala Leu Gln Thr Glu Ile Ala Asn Leu Leu Lys Glu
20 25 30

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Lys Glu Lys Leu Glu Phe Ile Leu Ala Ala His Gly Gly Cys
 35 40 45

<210> 61
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 <223> Description of Artificial Sequence: Primer
 <400> 61
 ccggaattca tgtgcggtgg tcggatcgcc cgg 33
 <210> 62
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 <223> Description of Artificial Sequence: Primer
 <400> 62
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 <210> 63
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 <223> Description of Artificial Sequence: Primer
 <400> 63
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 <210> 64
 <211> 38
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 <223> Description of Artificial Sequence: Primer
 <400> 64
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 <210> 65
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 <223> Description of Artificial Sequence: Primer
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<210> 66
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<210> 67
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 <223> Description of Artificial Sequence: Primer
 <400> 67
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<210> 68
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 <223> Description of Artificial Sequence: Primer
 <400> 68
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<210> 69
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 <212> DNA
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 <223> Description of Artificial Sequence: Primer
 <400> 69
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<210> 70
 <211> 39
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Description of Artificial Sequence: Primer
 <400> 70
 gtcgctaccg gcggctccgc aaccaacgtg gttcatgac 39

<210> 71
 <211> 31

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<212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Primer

 <400> 71
 ccggaattca tggacattga cccttataaa g 31

 <210> 72
 <211> 48
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Primer

 <400> 72
 cggaccaccg cagcccccac cggatccatt agtaccacc caggtagc 48

 <210> 73
 <211> 45
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Primer

 <400> 73
 gttggttcg gagccgcggg tagcgaccta gtagtcagtt atgtc 45

 <210> 74
 <211> 38
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Primer

 <400> 74
 cgcgccccaa gcttctacgg aagcgttgat aggatagg 38

 <210> 75
 <211> 33
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Primer

 <400> 75
 ctagccgcgg gttgcggtgg tcggatcgcc cgg 33

 <210> 76
 <211> 38
 <212> DNA
 <213> Artificial Sequence

10050398.011802

<220>
<223> Description of Artificial Sequence: Primer

<400> 76
cgcggtcccaa gcttttagca accaactggg ttcattgac 38

<210> 77
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 77
cggaattca tggccacact ttaaggagc 30

<210> 78
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 78
cgcggtcccaa gcttttagca accaactggg ttcattgac 38

<210> 79
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 79
cggaattca tggacattga cccttataaa g 31

<210> 80
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 80
cctagagcca cctttgccac catcttctaa attagtaccc acccaggtag c 51

<210> 81
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

10050893.011802

<400> 81
gaagatgggtg gcaaagggtg ctctagggtac ctagtagtca gttatgtc 48

<210> 82
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 82
cgcgccccaa gcttctaaac aacagtagtc tccggaag 38

<210> 83
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 83
gccgaattcc tagcagctag caccgaattt atctaa 36

<210> 84
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 84
ggttaagtgc acatgagagt gaaggagaaa tat 33

<210> 85
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 85
taaccgaatt caggaggtaa aaagatatgg 30

<210> 86
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 86
gaagtaaagc ttttaaccac cgcaaccacc agaag 35

10050888-011802

<210> 87
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 87
tcgaatgggc cctcatcttc gtgtgctagt cag

33

<210> 88
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Fos fusion
construct

<400> 88
Glu Phe Arg Arg
1

<210> 89
<211> 183
<212> PRT
<213> Hepatitis B virus

<400> 89
Met Asp Ile Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu
1 5 10 15

Ser Phe Leu Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp
20 25 30

Thr Ala Ser Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys
35 40 45

Ser Pro His His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu
50 55 60

Leu Met Thr Leu Ala Thr Trp Val Gly Gly Asn Leu Glu Asp Pro Ile
65 70 75 80

Ser Arg Asp Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys
85 90 95

Phe Arg Gln Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg
100 105 110

Glu Thr Val Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr
115 120 125

Pro Pro Ala Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro
130 135 140

Glu Thr Thr Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr
145 150 155 160

10050505.011002

Pro Ser Pro Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser
165 170 175

Gln Ser Arg Gly Ser Gln Cys
180

<210> 90

<211> 183

<212> PRT

<213> Hepatitis B virus

<400> 90

Met Asp Ile Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu
1 5 10 15

Ser Phe Leu Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp
20 25 30

Thr Ala Ser Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys
35 40 45

Ser Pro His His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu
50 55 60

Leu Met Thr Leu Ala Thr Trp Val Gly Gly Asn Leu Glu Asp Pro Thr
65 70 75 80

Ser Arg Asp Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys
85 90 95

Phe Arg Gln Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg
100 105 110

Glu Thr Val Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr
115 120 125

Pro Pro Ala Tyr Arg Pro Thr Asn Ala Pro Ile Leu Ser Thr Leu Pro
130 135 140

Glu Thr Cys Val Ile Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr
145 150 155 160

Pro Ser Pro Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser
165 170 175

Gln Ser Arg Gly Ser Gln Cys
180

<210> 91

<211> 212

<212> PRT

<213> Hepatitis B virus

<400> 91

Met Gln Leu Phe His Leu Cys Leu Ile Ile Ser Cys Ser Cys Pro Thr
1 5 10 15

Val Gln Ala Ser Lys Leu Cys Leu Gly Trp Leu Trp Gly Met Asp Ile
20 25 30

Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu

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35 40 45

Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp Thr Ala Ser
50 55 60

Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys Ser Pro His
65 70 75 80

His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu Leu Met Thr
85 90 95

Leu Ala Thr Trp Val Gly Gly Asn Leu Glu Asp Pro Ile Ser Arg Asp
100 105 110

Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys Phe Arg Gln
115 120 125

Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg Glu Thr Val
130 135 140

Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Pro Ala
145 150 155 160

Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro Glu Thr Thr
165 170 175

Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro
180 185 190

Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser Gln Ser Arg
195 200 205

Glu Ser Gln Cys
210

<210> 92
<211> 212
<212> PRT
<213> Hepatitis B virus

<400> 92
Met Gln Leu Phe His Leu Cys Leu Ile Ile Ser Cys Ser Cys Pro Thr
1 5 10 15

Val Gln Ala Ser Lys Leu Cys Leu Gly Trp Leu Trp Gly Met Asp Ile
20 25 30

Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu
35 40 45

Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp Asn Ala Ser
50 55 60

Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys Ser Pro His
65 70 75 80

His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu Leu Met Thr
85 90 95

Leu Ala Thr Trp Val Gly Gly Asn Leu Glu Asp Pro Ile Ser Arg Asp
100 105 110

Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys Phe Arg Gln

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115 120 125

Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg Glu Thr Val
130 135 140

Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Pro Ala
145 150 155 160

Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro Glu Thr Thr
165 170 175

Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro
180 185 190

Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser Gln Ser Arg
195 200 205

Glu Ser Gln Cys
210

<210> 93
<211> 183
<212> PRT
<213> Hepatitis B virus

<400> 93
Met Asp Ile Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu
1 5 10 15

Ser Phe Leu Pro Thr Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp
20 25 30

Thr Ala Ser Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys
35 40 45

Ser Pro His His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu
50 55 60

Leu Met Thr Leu Ala Thr Trp Val Gly Val Asn Leu Glu Asp Pro Ala
65 70 75 80

Ser Arg Asp Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys
85 90 95

Phe Arg Gln Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg
100 105 110

Glu Thr Val Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr
115 120 125

Pro Pro Ala Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro
130 135 140

Glu Thr Cys Val Val Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr
145 150 155 160

Pro Ser Pro Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser
165 170 175

Gln Ser Arg Glu Ser Gln Cys
180

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<210> 94
<211> 212
<212> PRT
<213> Hepatitis B virus

<400> 94
Met Gln Leu Phe His Leu Cys Leu Ile Ile Ser Cys Ser Cys Pro Thr
1 5 10 15
Val Gln Ala Ser Lys Leu Cys Leu Gly Trp Leu Trp Gly Met Asp Ile
20 25 30
Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu
35 40 45
Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp Thr Ala Ser
50 55 60
Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys Ser Pro His
65 70 75 80
His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Asp Leu Met Thr
85 90 95
Leu Ala Thr Trp Val Gly Gly Asn Leu Glu Asp Pro Val Ser Arg Asp
100 105 110
Leu Val Val Ser Tyr Val Asn Thr Asn Val Gly Leu Lys Phe Arg Gln
115 120 125
Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg Glu Thr Val
130 135 140
Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Pro Ala
145 150 155 160
Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro Glu Thr Thr
165 170 175
Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro
180 185 190
Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser Gln Ser Arg
195 200 205
Glu Ser Gln Cys
210

<210> 95
<211> 212
<212> PRT
<213> Hepatitis B virus

<400> 95
Met Gln Leu Phe His Leu Cys Leu Ile Ile Ser Cys Ser Cys Pro Thr
1 5 10 15
Val Gln Ala Ser Lys Leu Cys Leu Gly Trp Leu Trp Asp Met Asp Ile
20 25 30
Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu
35 40 45

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Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys Phe Arg Gln

115 120 125

Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg Glu Thr Val
130 135 140

Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Pro Ala
145 150 155 160

Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro Glu Thr Thr
165 170 175

Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro
180 185 190

Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser Gln Ser Arg
195 200 205

Glu Ser Gln Cys
210

<210> 97
<211> 212
<212> PRT
<213> Hepatitis B virus

<400> 97
Met Gln Leu Phe His Leu Cys Leu Ile Ile Ser Cys Ser Cys Pro Thr
1 5 10 15

Val Gln Ala Ser Lys Leu Cys Leu Gly Trp Leu Trp Gly Met Asp Ile
20 25 30

Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu
35 40 45

Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp Thr Ala Ser
50 55 60

Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys Ser Pro His
65 70 75 80

His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu Leu Met Thr
85 90 95

Leu Ala Thr Trp Val Gly Val Asn Leu Glu Asp Pro Ala Ser Arg Asp
100 105 110

Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys Phe Arg Gln
115 120 125

Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg Glu Thr Val
130 135 140

Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Pro Ala
145 150 155 160

Tyr Lys Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro Glu Thr Thr
165 170 175

Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro
180 185 190

Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser Gln Ser Arg

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205

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400> 99
Met Asp Ile Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu
  1          5          10          15
Ser Phe Leu Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp
      20          25          30
Thr Ala Ser Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys
      35          40          45

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Ser Pro His His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu
50 55 60

Leu Met Thr Leu Ala Thr Trp Val Gly Val Asn Leu Glu Asp Pro Ala
65 70 75 80

Ser Arg Asp Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys
85 90 95

Phe Arg Gln Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg
100 105 110

Glu Thr Val Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr
115 120 125

Pro Pro Ala Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro
130 135 140

Glu Thr Thr Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr
145 150 155 160

Pro Ser Pro Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Ser Ser
165 170 175

Gln Ser Arg Glu Ser Gln Cys
180

<210> 100
<211> 212
<212> PRT
<213> Hepatitis B virus

<400> 100
Met Gln Leu Phe His Leu Cys Leu Ile Ile Ser Cys Ser Cys Pro Thr
1 5 10 15

Val Gln Ala Ser Lys Leu Cys Leu Gly Trp Leu Trp Gly Met Asp Ile
20 25 30

Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu
35 40 45

Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp Thr Ala Ser
50 55 60

Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys Ser Pro His
65 70 75 80

His Thr Ala Leu Arg His Ala Ile Leu Cys Trp Gly Asp Leu Arg Thr
85 90 95

Leu Ala Thr Trp Val Gly Gly Asn Leu Glu Asp Pro Ile Ser Arg Asp
100 105 110

Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys Phe Arg Gln
115 120 125

Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg Glu Thr Val
130 135 140

Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Pro Ala

1050898.011002

145 150 155 160
 Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro Glu Thr Thr
 165 170 175
 Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro
 180 185 190
 Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser Gln Ser Arg
 195 200 205
 Glu Ser Gln Cys
 210

<210> 101
 <211> 212
 <212> PRT
 <213> Hepatitis B virus

<400> 101
 Met Gln Leu Phe His Leu Cys Leu Ile Ile Ser Cys Ser Cys Pro Thr
 1 5 10 15
 Val Gln Ala Ser Lys Leu Cys Leu Gly Trp Leu Trp Asp Met Asp Ile
 20 25 30
 Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu
 35 40 45
 Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp Thr Ala Ser
 50 55 60
 Ala Leu Phe Arg Asp Ala Leu Glu Ser Pro Glu His Cys Ser Pro His
 65 70 75 80
 His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu Leu Met Thr
 85 90 95
 Leu Ala Thr Trp Val Gly Ala Asn Leu Glu Asp Pro Ala Ser Arg Asp
 100 105
 Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys Phe Arg Gln
 115 120 125
 Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg Glu Thr Val
 130 135 140
 Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Gln Ala
 145 150 155 160
 Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro Glu Thr Cys
 165 170 175
 Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro
 180 185 190
 Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser Gln Ser Arg
 195 200 205
 Glu Ser Gln Cys
 210

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<210> 102
<211> 183
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic
human Hepatitis B construct

<400> 102
Met Asp Ile Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu
1 5 10 15
Ser Phe Leu Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp
20 25 30
Thr Ala Ser Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys
35 40 45
Ser Pro His His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu
50 55 60
Leu Met Thr Leu Ala Thr Trp Val Gly Val Asn Leu Glu Asp Pro Ala
65 70 75 80
Ser Arg Asp Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys
85 90 95
Phe Arg Gln Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg
100 105 110
Glu Thr Val Leu Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr
115 120 125
Pro Pro Ala Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro
130 135 140
Glu Thr Thr Val Val Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr
145 150 155 160
Pro Ser Pro Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser
165 170 175
Gln Ser Arg Glu Ser Gln Cys
180

<210> 103
<211> 212
<212> PRT
<213> Hepatitis B virus

<400> 103
Met Gln Leu Phe His Leu Cys Leu Ile Ile Ser Cys Ser Cys Pro Thr
1 5 10 15
Val Gln Ala Ser Lys Leu Cys Leu Gly Trp Leu Trp Gly Met Asp Ile
20 25 30
Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu
35 40 45
Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp Thr Ala Ser

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50 55 60

Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys Ser Pro His
65 70 75 80

His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Asp Leu Met Ser
85 90 95

Leu Ala Thr Trp Val Gly Val Asn Leu Glu Asp Pro Ile Ser Arg Asp
100 105 110

Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys Phe Arg Gln
115 120 125

Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg Glu Thr Val
130 135 140

Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Pro Ala
145 150 155 160

Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro Glu Thr Thr
165 170 175

Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro
180 185 190

Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser Gln Ser Arg
195 200 205

Glu Ser Gln Cys
210

<210> 104
<211> 183
<212> PRT
<213> Hepatitis B virus

<400> 104
Met Asp Ile Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu
1 5 10 15

Ser Phe Leu Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp
20 25 30

Thr Ala Ser Ala Leu Tyr Arg Asp Ala Leu Glu Ser Pro Glu His Cys
35 40 45

Ser Pro His His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu
50 55 60

Leu Met Thr Leu Ala Thr Trp Val Gly Val Asn Leu Glu Asp Pro Ala
65 70 75 80

Ser Arg Asp Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys
85 90 95

Phe Arg Gln Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg
100 105 110

Glu Thr Val Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr
115 120 125

Pro Pro Ala Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro

1050888-01302

130 135 140

Glu Thr Thr Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr
 145 150 155 160

Pro Ser Pro Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser
 165 170 175

Gln Ser Arg Glu Ser Gln Cys
 180

<210> 105
 <211> 183
 <212> PRT
 <213> Hepatitis B virus
 <400> 105

Met Asp Ile Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu
 1 5 10 15

Ser Phe Leu Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp
 20 25 30

Thr Ala Ser Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys
 35 40 45

Ser Pro His His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Asp
 50 55 60

Leu Met Thr Leu Ala Thr Trp Val Gly Val Asn Leu Glu Asp Pro Ala
 65 70 75 80

Ser Arg Asp Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys
 85 90 95

Phe Arg Gln Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg
 100 105 110

Glu Thr Val Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr
 115 120 125

Pro Pro Ala Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro
 130 135 140

Glu Thr Thr Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr
 145 150 155 160

Pro Ser Pro Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser
 165 170 175

Gln Ser Arg Glu Ser Gln Cys
 180

<210> 106
 <211> 183
 <212> PRT
 <213> Hepatitis B virus

<400> 106
 Met Asp Ile Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu
 1 5 10 15

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Ser Phe Leu Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp
20 25 30

Thr Ala Ser Ala Leu Tyr Arg Asp Ala Leu Glu Ser Pro Glu His Cys
35 40 45

Ser Pro His His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu
50 55 60

Leu Met Thr Leu Ala Thr Trp Val Gly Ala Asn Leu Glu Asp Pro Ala
65 70 75 80

Ser Arg Asp Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys
85 90 95

Phe Arg Gln Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg
100 105 110

Glu Thr Val Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr
115 120 125

Pro Pro Ala Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro
130 135 140

Glu Thr Thr Val Val Arg Arg Arg Gly Arg Thr Pro Arg Arg Arg Thr
145 150 155 160

Pro Ser Pro Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser
165 170 175

Gln Ser Arg Glu Ser Gln Cys
180

<210> 107
<211> 212
<212> PRT
<213> Hepatitis B virus

<400> 107
Met Gln Leu Phe His Leu Cys Leu Ile Ile Ser Cys Ser Cys Pro Thr
1 5 10 15

Val Gln Ala Ser Lys Leu Cys Leu Gly Trp Leu Trp Gly Met Asp Ile
20 25 30

Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu
35 40 45

Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp Thr Ala Ser
50 55 60

Ala Leu Tyr Arg Asp Ala Leu Glu Ser Pro Glu His Cys Ser Pro His
65 70 75 80

His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu Leu Met Thr
85 90 95

Leu Ala Thr Trp Val Gly Val Asn Leu Glu Asp Pro Ala Ser Arg Asp
100 105 110

Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys Phe Arg Gln
115 120 125

10050808.011002

Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg Glu Thr Val
130 135 140

Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Pro Ala
145 150 155 160

Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro Glu Thr Thr
165 170 175

Val Val Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro
180 185 190

Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser Gln Ser Arg
195 200 205

Glu Ser Gln Cys
210

<210> 108
<211> 212
<212> PRT
<213> Hepatitis B virus

<400> 108
Met Gln Leu Phe His Leu Cys Leu Ile Ile Ser Cys Ser Cys Pro Thr
1 5 10 15

Val Gln Ala Ser Lys Leu Cys Leu Gly Trp Leu Trp Gly Met Asp Ile
20 25 30

Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu
35 40 45

Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp Thr Ala Ser
50 55 60

Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys Ser Pro His
65 70 75 80

His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Asp Leu Met Thr
85 90 95

Leu Ala Thr Trp Val Gly Val Asn Leu Glu Asp Pro Ala Ser Arg Asp
100 105 110

Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys Phe Arg Gln
115 120 125

Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg Glu Thr Val
130 135 140

Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Pro Ala
145 150 155 160

Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro Glu Thr Thr
165 170 175

Val Val Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro
180 185 190

Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser Gln Ser Arg

10050808 011802

195 200 205

Glu Ser Gln Cys
210

<210> 109
<211> 212
<212> PRT
<213> Hepatitis B virus

<400> 109
Met Gln Leu Phe His Leu Cys Leu Ile Ile Ser Cys Thr Cys Pro Thr
1 5 10 15

Val Gln Ala Ser Lys Leu Cys Leu Gly Trp Leu Trp Gly Met Asp Ile
20 25 30

Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu
35 40 45

Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp Thr Ala Ser
50 55 60

Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys Ser Pro His
65 70 75 80

His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu Leu Met Thr
85 90 95

Leu Ala Thr Trp Val Gly Val Asn Leu Glu Asp Pro Ala Ser Arg Asp
100 105 110

Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys Phe Arg Gln
115 120 125

Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg Glu Thr Val
130 135 140

Ile Glu Tyr Leu Val Ala Phe Gly Val Trp Ile Arg Thr Pro Pro Ala
145 150 155 160

Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro Glu Thr Thr
165 170 175

Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro
180 185 190

Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser Gln Ser Arg
195 200 205

Glu Ser Gln Cys
210

<210> 110
<211> 212
<212> PRT
<213> Hepatitis B virus

<400> 110
Met Gln Leu Phe His Leu Cys Leu Ile Ile Ser Cys Ser Cys Pro Thr
1 5 10 15

1005000-011002

Val Gln Ala Ser Lys Leu Cys Leu Gly Trp Leu Trp Gly Met Asp Ile
20 25 30

Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu
35 40 45

Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp Thr Ala Ser
50 55 60

Ala Leu Tyr Arg Glu Ala Phe Glu Cys Ser Glu His Cys Ser Pro His
65 70 75 80

His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu Leu Met Thr
85 90 95

Leu Ala Thr Trp Val Gly Gly Asn Leu Glu Asp Pro Ile Ser Arg Asp
100 105 110

Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys Phe Arg Gln
115 120 125

Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg Glu Thr Val
130 135 140

Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Pro Ala
145 150 155 160

Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro Glu Thr Thr
165 170 175

Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro
180 185 190

Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser Gln Ser Arg
195 200 205

Glu Ser Gln Cys
210

<210> 111
<211> 212
<212> PRT
<213> Hepatitis B virus

<220>
<221> UNSURE
<222> (28)
<223> May be any amino acid.

<400> 111
Met Gln Leu Phe His Leu Cys Leu Ile Ile Ser Cys Ser Cys Pro Thr
1 5 10 15

Val Gln Ala Ser Lys Leu Cys Leu Gly Trp Leu Xaa Asp Met Asp Ile
20 25 30

Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu
35 40 45

Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp Thr Ala Ser

10030368-011602

50 55 60

Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys Ser Pro His
65 70 75 80

His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Asp Leu Ile Thr
85 90 95

Leu Ser Thr Trp Val Gly Gly Asn Leu Glu Asp Pro Thr Ser Arg Asp
100 105 110

Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys Phe Arg Gln
115 120 125

Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg Glu Thr Val
130 135 140

Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Pro Ala
145 150 155 160

Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro Glu Thr Thr
165 170 175

Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro
180 185 190

Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Thr Gln Ser Arg
195 200 205

Glu Ser Gln Cys
210

<210> 112
<211> 212
<212> PRT
<213> Hepatitis B virus

<400> 112
Met Gln Leu Phe His Leu Cys Leu Ile Ile Ser Cys Ser Cys Pro Thr
1 5 10 15

Val Gln Ala Ser Lys Leu Cys Leu Gly Trp Leu Trp Gly Met Asp Ile
20 25 30

Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu
35 40 45

Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp Asn Ala Ser
50 55 60

Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys Ser Pro His
65 70 75 80

His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu Leu Met Thr
85 90 95

Leu Ala Thr Trp Val Gly Val Asn Leu Glu Asp Pro Ala Ser Arg Asp
100 105 110

Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys Phe Arg Gln
115 120 125

Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg Glu Thr Val

10050808.011802

130 135 140

Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Pro Ala
145 150 155 160

Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro Glu Thr Thr
165 170 175

Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro
180 185 190

Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser Gln Ser Arg
195 200 205

Glu Ser Gln Cys
210

<210> 113
<211> 212
<212> PRT
<213> Hepatitis B virus

<400> 113
Met Gln Leu Phe His Leu Cys Leu Ile Ile Ser Cys Ser Cys Pro Thr
1 5 10 15

Val Gln Ala Ser Lys Leu Cys Leu Gly Trp Leu Trp Gly Met Asp Ile
20 25 30

Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu
35 40 45

Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp Thr Ala Ser
50 55 60

Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys Ser Pro His
65 70 75 80

His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu Leu Met Thr
85 90 95

Leu Ala Thr Trp Val Gly Val Asn Leu Glu Asp Pro Ala Ser Arg Asp
100 105 110

Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys Phe Arg Gln
115 120 125

Leu Leu Trp Phe His Ile Cys Cys Leu Thr Phe Gly Arg Glu Thr Val
130 135 140

Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Pro Ala
145 150 155 160

Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro Glu Thr Thr
165 170 175

Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro
180 185 190

Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser Gln Ser Arg
195 200 205

Glu Ser Gln Cys

10050393.011802

210

<210> 114
<211> 212
<212> PRT
<213> Hepatitis B virus

<400> 114
Met Gln Leu Phe His Leu Cys Leu Ile Ile Ser Cys Ser Cys Pro Thr
1 5 10 15
Val Gln Ala Ser Lys Leu Cys Leu Gly Trp Leu Trp Gly Met Asp Ile
20 25 30
Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu
35 40 45
Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp Thr Ala Ser
50 55 60
Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys Ser Pro His
65 70 75 80
His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu Leu Met Thr
85 90 95
Leu Ala Thr Trp Val Gly Val Asn Leu Glu Asp Pro Ala Ser Arg Asp
100 105 110
Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys Phe Arg Gln
115 120 125
Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg Glu Thr Val
130 135 140
Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Pro Ala
145 150 155 160
Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro Glu Thr Thr
165 170 175
Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro
180 185 190
Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser Gln Ser Arg
195 200 205
Glu Pro Gln Cys
210

<210> 115
<211> 212
<212> PRT
<213> Hepatitis B virus

<400> 115
Met Gln Leu Phe His Leu Cys Leu Ile Ile Ser Cys Ser Cys Pro Thr
1 5 10 15
Val Gln Ala Ser Lys Leu Cys Leu Gly Trp Leu Trp Gly Met Asp Ile
20 25 30

10050808 011001

Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu
35 40 45

Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Ser Thr Ala Ser
50 55 60

Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys Ser Pro His
65 70 75 80

His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu Leu Met Thr
85 90 95

Leu Ala Thr Trp Val Gly Val Asn Leu Glu Asp Pro Ala Ser Arg Asp
100 105 110

Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys Phe Arg Gln
115 120 125

Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg Glu Thr Val
130 135 140

Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Pro Ala
145 150 155 160

Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro Glu Thr Thr
165 170 175

Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro
180 185 190

Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser Gln Ser Arg
195 200 205

Glu Ser Gln Cys
210

<210> 116
<211> 212
<212> PRT
<213> Hepatitis B virus

<400> 116
Met Gln Leu Phe His Leu Cys Leu Ile Ile Ser Cys Ser Cys Pro Thr
1 5 10 15

Val Gln Ala Ser Lys Leu Cys Leu Gly Trp Leu Trp Gly Met Asp Ile
20 25 30

Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu
35 40 45

Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp Thr Ala Ser
50 55 60

Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys Ser Pro His
65 70 75 80

His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu Leu Met Thr
85 90 95

Leu Ala Thr Trp Val Gly Val Asn Leu Glu Asp Pro Ala Ser Arg Asp

10650000-074302

100 105 110

Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys Phe Arg Gln
115 120 125

Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg Glu Thr Val
130 135 140

Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Pro Ala
145 150 155 160

Tyr Arg Pro Pro Asn Ala Pro Ile Leu Leu Thr Leu Pro Glu Thr Thr
165 170 175

Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro
180 185 190

Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser Gln Ser Arg
195 200 205

Glu Ser Gln Cys
210

<210> 117
<211> 212
<212> PRT
<213> Hepatitis B virus

<400> 117
Met Gln Leu Phe His Leu Cys Leu Ile Ile Ser Cys Ser Cys Pro Thr
1 5 10 15

Val Gln Ala Ser Lys Leu Cys Leu Gly Trp Leu Trp Gly Met Asp Ile
20 25 30

Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu
35 40 45

Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp Thr Ala Ser
50 55 60

Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys Ser Pro His
65 70 75 80

His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Asp Leu Met Thr
85 90 95

Leu Ala Thr Trp Val Gly Val Asn Leu Glu Asp Pro Ala Ser Arg Asp
100 105 110

Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys Phe Lys Gln
115 120 125

Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg Glu Thr Val
130 135 140

Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Pro Ala
145 150 155 160

Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro Glu Thr Thr
165 170 175

Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro

10050888-011602

180 185 190

Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser Gln Ser Arg
195 200 205

Glu Ser Gln Cys
210

<210> 118
<211> 212
<212> PRT
<213> Hepatitis B virus

<400> 118

Met Gln Leu Phe His Leu Cys Leu Ile Ile Ser Cys Ser Cys Pro Thr
1 5 10 15

Val Gln Ala Ser Lys Leu Cys Leu Gly Trp Leu Trp Gly Met Asp Ile
20 25 30

Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu
35 40 45

Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp Thr Ala Ala
50 55 60

Ala Leu Tyr Arg Asp Ala Leu Glu Ser Pro Glu His Cys Ser Pro His
65 70 75 80

His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu Leu Met Thr
85 90 95

Leu Ala Thr Trp Val Gly Thr Asn Leu Glu Asp Pro Ala Ser Arg Asp
100 105 110

Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys Phe Arg Gln
115 120 125

Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg Glu Thr Val
130 135 140

Leu Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Pro Ala
145 150 155 160

Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro Glu Thr Thr
165 170 175

Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro
180 185 190

Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser Gln Ser Arg
195 200 205

Glu Ser Gln Cys
210

<210> 119
<211> 183
<212> PRT
<213> Hepatitis B virus

10050008-011002

<400> 119

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Met Asp Ile Asp Pro Tyr Lys Glu Phe Gly Ala Ser Met Glu Leu Leu
 1           5           10           15

Ser Phe Leu Pro Ser Asp Phe Tyr Pro Ser Val Arg Asp Leu Leu Asp
          20           25           30

Thr Ala Ser Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys
          35           40           45

Thr Pro His His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu
          50           55           60

Leu Met Thr Leu Ala Thr Trp Val Gly Gly Asn Leu Gln Asp Pro Thr
          65           70           75           80

Ser Arg Asp Leu Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys
          85           90           95

Phe Arg Gln Leu Leu Trp Phe His Val Ser Cys Leu Thr Phe Gly Arg
          100          105          110

Glu Thr Val Val Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr
          115          120          125

Pro Gln Ala Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro
          130          135          140

Glu Thr Cys Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr
          145          150          155          160

Pro Ser Pro Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser
          165          170          175

Gln Ser Arg Glu Ser Gln Cys
          180

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<210> 120

<211> 183

<212> PRT

<213> Hepatitis B virus

<400> 120

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Met Asp Ile Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu
 1           5           10           15

Ser Phe Leu Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp
          20           25           30

Thr Ala Ser Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys
          35           40           45

Ser Pro His His Thr Ala Leu Arg His Val Phe Leu Cys Trp Gly Asp
          50           55           60

Leu Met Thr Leu Ala Thr Trp Val Gly Gly Asn Leu Glu Asp Pro Thr
          65           70           75           80

Ser Arg Asp Leu Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys
          85           90           95

Phe Arg Gln Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg

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10050898-011802

100 105 110

Glu Thr Val Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr
115 120 125

Pro Pro Ala Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro
130 135 140

Glu Thr Thr Val Val Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr
145 150 155 160

Pro Ser Pro Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser
165 170 175

Gln Ser Arg Glu Ser Gln Cys
180

<210> 121
<211> 212
<212> PRT
<213> Hepatitis B virus

<400> 121
Met Gln Leu Phe His Leu Cys Leu Ile Ile Ser Cys Ser Cys Pro Thr
1 5 10 15

Val Gln Ala Ser Lys Leu Cys Leu Gly Trp Leu Trp Gly Met Asp Ile
20 25 30

Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu
35 40 45

Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp Thr Ala Ser
50 55 60

Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys Ser Pro His
65 70 75 80

His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Asp Leu Thr Thr
85 90 95

Leu Ala Thr Trp Val Gly Val Asn Leu Glu Asp Pro Ala Ser Arg Asp
100 105 110

Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys Phe Arg Gln
115 120 125

Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg Glu Thr Val
130 135 140

Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Pro Ala
145 150 155 160

Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro Glu Thr Thr
165 170 175

Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro
180 185 190

Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser Gln Ser Arg
195 200 205

Glu Ser Gln Cys

1050333.014002

210

<210> 122
<211> 212
<212> PRT
<213> Hepatitis B virus

<400> 122
Met Gln Leu Phe His Leu Cys Leu Ile Ile Ser Cys Ser Cys Pro Thr
1 5 10 15
Val Gln Ala Ser Lys Leu Cys Leu Gly Trp Leu Trp Gly Met Asp Ile
20 25 30
Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu
35 40 45
Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp Thr Ala Ser
50 55 60
Ala Leu Tyr Arg Asp Ala Leu Glu Ser Pro Glu His Cys Ser Pro His
65 70 75 80
His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu Leu Met Thr
85 90 95
Leu Ala Thr Trp Val Gly Val Asn Leu Glu Asp Pro Ala Ser Arg Asp
100 105 110
Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys Phe Arg Gln
115 120 125
Leu Leu Trp Phe His Ile Ser Cys Leu Ile Phe Gly Arg Glu Thr Val
130 135 140
Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Pro Ala
145 150 155 160
Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro Glu Thr Thr
165 170 175
Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro
180 185 190
Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser Gln Ser Arg
195 200 205
Glu Ser Gln Cys
210

<210> 123
<211> 183
<212> PRT
<213> Hepatitis B virus

<400> 123
Met Asp Ile Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu
1 5 10 15
Ser Phe Leu Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp
20 25 30

105033-01302

Thr Ala Ser Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys
35 40 45

Ser Pro His His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Asp
50 55 60

Leu Met Thr Leu Ala Thr Trp Val Gly Val Asn Leu Glu Asp Pro Val
65 70 75 80

Ser Arg Asp Leu Val Val Ser Tyr Val Asn Thr Asn Val Gly Leu Lys
85 90 95

Phe Arg Gln Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg
100 105 110

Glu Thr Val Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr
115 120 125

Pro Pro Ala Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro
130 135 140

Glu Thr Thr Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr
145 150 155 160

Pro Ser Pro Ala Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser
165 170 175

Gln Ser Arg Glu Ser Gln Cys
180

<210> 124
<211> 212
<212> PRT
<213> Hepatitis B virus

<400> 124
Met Gln Leu Phe His Leu Cys Leu Ile Ile Ser Cys Ser Cys Pro Thr
1 5 10 15

Val Gln Ala Ser Lys Leu Cys Leu Gly Trp Leu Trp Gly Met Asp Ile
20 25 30

Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu
35 40 45

Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp Thr Ala Ser
50 55 60

Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys Ser Pro His
65 70 75 80

His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Asp Leu Met Asn
85 90 95

Leu Ala Thr Trp Val Gly Gly Asn Leu Glu Asp Pro Val Ser Arg Asp
100 105 110

Leu Val Val Gly Tyr Val Asn Thr Thr Val Gly Leu Lys Phe Arg Gln
115 120 125

Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg Glu Thr Val

10050888-011802

130 135 140

Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Pro Ala
145 150 155 160

Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro Glu Thr Thr
165 170 175

Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro
180 185 190

Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser Gln Ser Arg
195 200 205

Glu Ser Gln Cys
210

<210> 125
<211> 183
<212> PRT
<213> Hepatitis B virus

<400> 125
Met Asp Ile Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu
1 5 10 15

Ser Phe Leu Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp
20 25 30

Thr Ala Ser Ala Leu Tyr Arg Asp Ala Leu Glu Ser Pro Glu His Cys
35 40 45

Ser Pro His His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Asp
50 55 60

Leu Met Thr Leu Ala Thr Trp Val Gly Val Asn Leu Glu Asp Pro Ala
65 70 75 80

Ser Arg Asp Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys
85 90 95

Phe Arg Gln Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg
100 105 110

Glu Thr Val Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr
115 120 125

Pro Pro Ala Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro
130 135 140

Glu Thr Thr Val Val Arg Arg Arg Gly Arg Thr Pro Arg Arg Arg Thr
145 150 155 160

Pro Ser Pro Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser
165 170 175

Gln Ser Arg Glu Ser Gln Cys
180

<210> 126
<211> 212
<212> PRT

10050366-011001

<213> Hepatitis B virus

<400> 126

Met Gln Leu Phe His Leu Cys Leu Ile Ile Ser Cys Ser Cys Pro Thr
1 5 10 15

Val Gln Ala Ser Lys Leu Cys Leu Gly Trp Leu Trp Gly Met Asp Ile
20 25 30

Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu
35 40 45

Pro Ser Asp Phe Phe Pro Ser Val Arg Ala Leu Leu Asp Thr Ala Ser
50 55 60

Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys Ser Pro His
65 70 75 80

His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu Leu Met Thr
85 90 95

Leu Ala Thr Trp Val Gly Val Asn Leu Glu Asp Pro Ala Ser Arg Asp
100 105 110

Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys Phe Arg Gln
115 120 125

Ile Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg Glu Thr Val
130 135 140

Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Pro Ala
145 150 155 160

Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro Glu Thr Thr
165 170 175

Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro
180 185 190

Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser Gln Ser Arg
195 200 205

Glu Ser Gln Cys
210

<210> 127

<211> 212

<212> PRT

<213> Hepatitis B virus

<400> 127

Met Gln Leu Phe His Leu Cys Leu Ile Ile Ser Cys Ser Cys Pro Thr
1 5 10 15

Val Gln Ala Ser Lys Leu Cys Leu Gly Trp Leu Trp Gly Met Asp Ile
20 25 30

Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu
35 40 45

Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp Thr Ala Ser
50 55 60

20050803.044002

Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys Ser Pro His
65 70 75 80

His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Asp Leu Met Thr
85 90 95

Leu Ala Thr Trp Val Gly Val Asn Leu Glu Asp Pro Ala Thr Arg Asp
100 105 110

Leu Val Val Ser Tyr Val Asn Thr Asn Val Gly Leu Lys Phe Arg Gln
115 120 125

Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg Glu Thr Val
130 135 140

Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Pro Ala
145 150 155 160

Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro Glu Thr Thr
165 170 175

Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro
180 185 190

Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser Gln Ser Arg
195 200 205

Glu Ser Gln Cys
210

<210> 128
<211> 212
<212> PRT
<213> Hepatitis B virus

<400> 128
Met Gln Leu Phe His Leu Cys Leu Ile Ile Ser Cys Ser Cys Pro Thr
1 5 10 15

Val Gln Ala Ser Lys Leu Cys Leu Gly Trp Leu Trp Gly Met Asp Ile
20 25 30

Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu
35 40 45

Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp Thr Ala Ser
50 55 60

Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys Ser Pro His
65 70 75 80

His Thr Ala Leu Arg Gln Arg Ile Leu Cys Trp Gly Glu Leu Met Thr
85 90 95

Leu Ala Thr Trp Val Gly Val Asn Leu Glu Asp Pro Ala Ser Arg Asp
100 105 110

Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys Phe Arg Gln
115 120 125

Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg Glu Thr Val

0050889-011802

130					135					140					
Ile	Glu	Tyr	Leu	Val	Ser	Phe	Gly	Val	Trp	Ile	Arg	Thr	Pro	Pro	Ala
145					150					155					160
Tyr	Arg	Pro	Pro	Asn	Ala	Pro	Ile	Leu	Ser	Thr	Leu	Pro	Glu	Thr	Thr
				165					170					175	
Val	Val	Arg	Arg	Arg	Gly	Arg	Ser	Pro	Arg	Arg	Arg	Thr	Pro	Ser	Pro
				180				185					190		
Arg	Arg	Arg	Arg	Ser	Gln	Ser	Pro	Arg	Arg	Thr	Arg	Ser	Gln	Ser	Arg
				195			200					205			
Glu	Ser	Gln	Cys												
				210											
<210> 129															
<211> 212															
<212> PRT															
<213> Hepatitis B virus															
<400> 129															
Met	Gln	Leu	Phe	His	Leu	Cys	Leu	Val	Ile	Ser	Cys	Ser	Cys	Pro	Thr
1				5					10					15	
Val	Gln	Ala	Ser	Lys	Leu	Cys	Leu	Gly	Trp	Leu	Trp	Gly	Met	Asp	Ile
			20					25					30		
Asp	Pro	Tyr	Lys	Glu	Phe	Gly	Ala	Thr	Val	Glu	Leu	Leu	Ser	Phe	Leu
			35				40						45		
Pro	Ser	Asp	Phe	Phe	Pro	Ser	Val	Arg	Asp	Leu	Leu	Asp	Thr	Ala	Ala
						55						60			
Ala	Leu	Tyr	Arg	Glu	Ala	Leu	Glu	Ser	Pro	Glu	His	Cys	Ser	Pro	His
65				70						75					80
His	Thr	Ala	Leu	Arg	Gln	Ala	Ile	Leu	Cys	Trp	Gly	Glu	Leu	Met	Thr
				85					90					95	
Leu	Ala	Thr	Trp	Val	Gly	Asn	Asn	Leu	Glu	Asp	Pro	Ala	Ser	Arg	Asp
			100					105					110		
Leu	Val	Val	Asn	Tyr	Val	Asn	Thr	Asn	Met	Gly	Leu	Lys	Ile	Arg	Gln
			115				120					125			
Leu	Leu	Trp	Phe	His	Ile	Ser	Cys	Leu	Thr	Phe	Gly	Arg	Glu	Thr	Val
					135						140				
Leu	Glu	Tyr	Leu	Val	Ser	Phe	Gly	Val	Trp	Ile	Arg	Thr	Pro	Pro	Ala
145					150					155					160
Tyr	Arg	Pro	Pro	Asn	Ala	Pro	Ile	Leu	Ser	Thr	Leu	Pro	Glu	Thr	Thr
				165					170					175	
Val	Val	Arg	Arg	Arg	Gly	Arg	Ser	Pro	Arg	Arg	Arg	Thr	Pro	Ser	Pro
				180				185					190		
Arg	Arg	Arg	Arg	Ser	Gln	Ser	Pro	Arg	Arg	Arg	Arg	Ser	Gln	Ser	Arg
				195			200					205			
Glu	Ser	Gln	Cys												

210

<210> 130
<211> 212
<212> PRT
<213> Hepatitis B virus

<400> 130
Met Gln Leu Phe His Leu Cys Leu Ile Ile Ser Cys Ser Cys Pro Thr
1 5 10 15
Val Gln Ala Ser Lys Leu Cys Leu Gly Trp Leu Trp Gly Met Asp Ile
20 25 30
Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu Ser Phe Leu
35 40 45
Pro Ser Ala Phe Phe Pro Ser Val Arg Asp Leu Leu Asp Thr Ala Ser
50 55 60
Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys Ser Pro His
65 70 75 80
His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Asp Leu Met Thr
85 90 95
Leu Ala Thr Trp Val Gly Val Asn Leu Glu Asp Pro Ala Ser Arg Asp
100 105 110
Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys Phe Arg Gln
115 120 125
Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg Glu Thr Val
130 135 140
Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Pro Ala
145 150 155 160
Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro Glu Thr Thr
165 170 175
Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro
180 185 190
Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser Gln Ser Arg
195 200 205
Glu Ser Gln Cys
210

<210> 131
<211> 183
<212> PRT
<213> Hepatitis B virus

<400> 131
Met Asp Ile Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu
1 5 10 15
Ser Phe Leu Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp
20 25 30

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Thr Ala Ala Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys
 35 40 45

Ser Pro His His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu
 50 55 60

Leu Met Thr Leu Ala Thr Trp Val Gly Asn Asn Leu Glu Asp Pro Ala
 65 70 75 80

Ser Arg Asp Leu Val Val Asn Tyr Val Asn Thr Asn Met Gly Leu Lys
 85 90 95

Ile Arg Gln Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg
 100 105 110

Glu Thr Val Leu Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr
 115 120 125

Pro Pro Ala Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro
 130 135 140

Glu Thr Thr Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr
 145 150 155 160

Pro Ser Pro Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser
 165 170 175

Gln Ser Arg Glu Ser Gln Cys
 180

<210> 132

<211> 183

<212> PRT

<213> Hepatitis B virus

<400> 132

Met Asp Ile Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu
 1 5 10 15

Ser Phe Leu Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp
 20 25 30

Thr Ala Ser Ala Leu Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys
 35 40 45

Ser Pro His His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu
 50 55 60

Leu Met Thr Leu Ala Thr Trp Val Gly Gly Asn Leu Glu Asp Pro Ile
 65 70 75 80

Ser Arg Asp Leu Val Val Ser Tyr Val Asn Thr Asn Met Gly Leu Lys
 85 90 95

Phe Arg Gln Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg
 100 105 110

Glu Thr Val Ile Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr
 115 120 125

Pro Pro Ala Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro

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130 135 140

Glu Thr Cys Val Val Arg Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr
 145 150 155 160

Pro Ser Pro Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Arg Ser
 165 170 175

Gln Ser Arg Gly Ser Gln Cys
 180

<210> 133
 <211> 3221
 <212> DNA
 <213> Hepatitis B virus

<220>
 <221> CDS
 <222> (1901)..(2458)

<400> 133
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 aggacccctg ctctgtgtac aggcgggggtt tttattgttg acaagaatcc tcacaatacc 240
 gcagagtcta gactcgtggt ggaattctct caattttata gggggatcac ccgtgtgtct 300
 tggccaaat tcgcagtc ccacctccaa tcactcacca acctcctgtc ctccaatttg 360
 tcctggttat cgctggatgt gtctgcggcg ttttatcata ttctcttca tcctgctgct 420
 atgectcate ttcttattgg ttctcttga ttatcaaggt atgttgccg tttgtcctct 480
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 aggcaactct atgtttccct catgttgctg tacaaaacct acgggttgaa attgcacctg 600
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 tgtttggcct tcagctatat ggatgatgtg gtattggggg ccaagtcgtg acagcatcgt 780
 gagtcccttt ataccgtgtg taccaatttt cttttgtctc tgggtatata tttaaacct 840
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 gttacaggcg ctattgattg gaaagtatgt caaagaattg tgggtctttt gggctttgct 1020
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 aaacaggcct tcactttctc gccaaacttac aaggccttct taagtaacaa gtacatgaac 1140
 ctttaccctg ttgctcgga acggcctggt ctgtgccaag tgtttgctga cgcaaccccc 1200
 actggttggg gcttggccat agggccatcag cgcattgagt gaacctttgt ggctcctctg 1260

10050888 011000

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ctaggctgta ctgccaactg gatccttcgc gggacgtcct ttgtttacgt cccgtcggtg 1440
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ctgcggttcc agccgaccac ggggcgacc tctctttacg cggctcccc gtctgtgect 1560
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gcgcaccagc accatgcaac tttttcacct ctgcctaact atctcttgta catgtccacc 1860
tgttcaagcc tccaagctgt gccttgggtg gctttggggc atg gac att gac cct 1915
Met Asp Ile Asp Pro
1 5
tat aaa gaa ttt gga gct act gtg gag tta ctc tcg ttt ttg cct tct 1963
Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Ser Phe Leu Pro Ser
10 15 20
gac ttc ttt cct tcc gtc aga gat ctc cta gac acc gcc tca gct ctg 2011
Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp Thr Ala Ser Ala Leu
25 30 35
tat cga gaa gcc tta gag tct cct gag cat tgc tca cct cac cat act 2059
Tyr Arg Glu Ala Leu Glu Ser Pro Glu His Cys Ser Pro His His Thr
40 45 50
gca ctc agg caa gcc att ctc tgc tgg ggg gaa ttg atg act cta gct 2107
Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Glu Leu Met Thr Leu Ala
55 60 65
acc tgg gtg ggt aat aat ttg gaa gat cca gca tcc agg gat cta gta 2155
Thr Trp Val Gly Asn Asn Leu Glu Asp Pro Ala Ser Arg Asp Leu Val
70 75 80 85
gtc aat tat gtt aat act aac atg ggt tta aag atc agg caa cta ttg 2203
Val Asn Tyr Val Asn Thr Asn Met Gly Leu Lys Ile Arg Gln Leu Leu
90 95 100
tgg ttt cat ata tct tgc ctt act ttt gga aga gag act gta ctt gaa 2251
Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg Glu Thr Val Leu Glu
105 110 115
tat ttg gtc tct ttc gga gtg tgg att cgc act cct cca gcc tat aga 2299
Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Pro Ala Tyr Arg
120 125 130
cca cca aat gcc cct atc tta tca aca ctt cgg gaa act act gtt gtt 2347
Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro Glu Thr Thr Val Val
135 140 145
aga cga cgg gac cga ggc agg tcc cct aga aga aga act ccc tgc cct 2395
Arg Arg Arg Asp Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro
150 155 160 165

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gaa tct caa tgt tag tattccttgg actcataagg tgggaaactt tactgggctt 2498
Glu Ser Gln Cys
185

tattctctcta	cagtacctat	ctttaatcct	gaatggcaaa	ctccttcctt	tcctaagatt	2558
catttacaag	aggacattat	tgataggtgt	caacaatttg	tggggccctct	cactgtaaat	2618
gaaaagagaa	gattgaaatt	aattatgcct	gctagattct	atcctacca	cactaaatat	2678
ttgcccttag	acaaaggaat	taaaccttat	tatccagatc	aggtagttaa	tcattacttc	2738
caaacacag	attattttaca	tactcttttg	aaggctggta	ttctatataa	gagggaaacc	2798
acacgtagcg	catcattttg	cgggtcacca	tattcttggg	aacaagagct	acagcatggg	2858
aggttggtga	ttaaaacctc	gcaaaggcat	ggggacgaat	ctttctgttc	ccaacctctt	2918
gggattcttt	cccgatcatc	agttggacc	tgcatctgga	gccaaactca	acaatccaga	2978
ttgggacttc	aaceccatca	aggaccactg	gccagcagcc	aaccaggtag	gagtgggagc	3038
attcgggcca	gggctcaccc	ctccacacgg	cggtattttg	gggtggagcc	ctcaggctca	3098
gggcataattg	accacagtgt	caacaattcc	tctctctgcc	tccaccaate	ggcagtcagg	3158
aaggcagcct	actcccatct	ctccacctct	aagagacagt	catcctcagg	ccatgcagtg	3218
gaa						3221

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<210> 134
<211> 185
<212> PRT
<213> Hepatitis B virus
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Met	Asp	Ile	Asp	Pro	Tyr	Lys	Glu	Phe	Gly	Ala	Thr	Val	Glu	Leu	Leu
1				5					10					15	
Ser	Phe	Leu	Pro	Ser	Asp	Phe	Phe	Pro	Ser	Val	Arg	Asp	Leu	Leu	Asp
			20					25					30		
Thr	Ala	Ser	Ala	Leu	Tyr	Arg	Glu	Ala	Leu	Glu	Ser	Pro	Glu	His	Cys
		35					40					45			
Ser	Pro	His	His	Thr	Ala	Leu	Arg	Gln	Ala	Ile	Leu	Cys	Trp	Gly	Glu
	50					55					60				
Leu	Met	Thr	Leu	Ala	Thr	Trp	Val	Gly	Asn	Asn	Leu	Glu	Asp	Pro	Ala
65				70						75				80	
Ser	Arg	Asp	Leu	Val	Val	Asn	Tyr	Val	Asn	Thr	Asn	Met	Gly	Leu	Lys
				85					90					95	
Ile	Arg	Gln	Leu	Leu	Trp	Phe	His	Ile	Ser	Cys	Leu	Thr	Phe	Gly	Arg
			100					105					110		
Glu	Thr	Val	Leu	Glu	Tyr	Leu	Val	Ser	Phe	Gly	Val	Trp	Ile	Arg	Thr
		115					120					125			
Pro	Pro	Ala	Tyr	Arg	Pro	Pro	Asn	Ala	Pro	Ile	Leu	Ser	Thr	Leu	Pro
		130				135					140				
Glu	Thr	Thr	Val	Val	Arg	Arg	Arg	Asp	Arg	Gly	Arg	Ser	Pro	Arg	Arg
145					150					155				160	
Arg	Thr	Pro	Ser	Pro	Arg	Arg	Arg	Arg	Ser	Gln	Ser	Pro	Arg	Arg	Arg
				165					170					175	

Arg Ser Gln Ser Arg Glu Ser Gln Cys
180 185

<210> 135
<211> 188
<212> PRT
<213> Woodchuck hepatitis B virus

<400> 135
Met Asp Ile Asp Pro Tyr Lys Glu Phe Gly Ser Ser Tyr Gln Leu Leu
1 5 10 15
Asn Phe Leu Pro Leu Asp Phe Phe Pro Asp Leu Asn Ala Leu Val Asp
20 25 30
Thr Ala Thr Ala Leu Tyr Glu Glu Leu Thr Gly Arg Glu His Cys
35 40 45
Ser Pro His His Thr Ala Ile Arg Gln Ala Leu Val Cys Trp Asp Glu
50 55 60
Leu Thr Lys Leu Ile Ala Trp Met Ser Ser Asn Ile Thr Ser Glu Gln
65 70 75 80
Val Arg Thr Ile Ile Val Asn His Val Asn Asp Thr Trp Gly Leu Lys
85 90 95
Val Arg Gln Ser Leu Trp Phe His Leu Ser Cys Leu Thr Phe Gly Gln
100 105 110
His Thr Val Gln Glu Phe Leu Val Ser Phe Gly Val Trp Ile Arg Thr
115 120 125
Pro Ala Pro Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro
130 135 140
Glu His Thr Val Ile Arg Arg Arg Gly Gly Ala Arg Ala Ser Arg Ser
145 150 155 160
Pro Arg Arg Arg Thr Pro Ser Pro Arg Arg Arg Arg Ser Gln Ser Pro
165 170 175
Arg Arg Arg Arg Ser Gln Ser Pro Ser Thr Asn Cys
180 185

<210> 136
<211> 217
<212> PRT
<213> Ground squirrel hepatitis virus

<400> 136
Met Tyr Leu Phe His Leu Cys Leu Val Phe Ala Cys Val Pro Cys Pro
1 5 10 15
Thr Val Gln Ala Ser Lys Leu Cys Leu Gly Trp Leu Trp Asp Met Asp
20 25 30
Ile Asp Pro Tyr Lys Glu Phe Gly Ser Ser Tyr Gln Leu Asn Phe
35 40 45
Leu Pro Leu Asp Phe Phe Pro Asp Leu Asn Ala Leu Val Asp Thr Ala

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50 55 60

Ala Ala Leu Tyr Glu Glu Glu Leu Thr Gly Arg Glu His Cys Ser Pro
65 70 75 80

His His Thr Ala Ile Arg Gln Ala Leu Val Cys Trp Glu Glu Leu Thr
85 90 95

Arg Leu Ile Thr Trp Met Ser Glu Asn Thr Thr Glu Glu Val Arg Arg
100 105 110

Ile Ile Val Asp His Val Asn Asn Thr Trp Gly Leu Lys Val Arg Gln
115 120 125

Thr Leu Trp Phe His Leu Ser Cys Leu Thr Phe Gly Gln His Thr Val
130 135 140

Gln Glu Phe Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Ala Pro
145 150 155 160

Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro Glu His Thr
165 170 175

Val Ile Arg Arg Arg Gly Gly Ser Arg Ala Ala Arg Ser Pro Arg Arg
180 185 190

Arg Thr Pro Ser Pro Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg
195 200 205

Arg Ser Gln Ser Pro Ala Ser Asn Cys
210 215

<210> 137
<211> 262
<212> PRT
<213> Snow Goose Hepatitis B Virus

<400> 137
Met Asp Val Asn Ala Ser Arg Ala Leu Ala Asn Val Tyr Asp Leu Pro
1 5 10 15

Asp Asp Phe Phe Pro Lys Ile Glu Asp Leu Val Arg Asp Ala Lys Asp
20 25 30

Ala Leu Glu Pro Tyr Trp Lys Ser Asp Ser Ile Lys Lys His Val Leu
35 40 45

Ile Ala Thr His Phe Val Asp Leu Ile Glu Asp Phe Trp Gln Thr Thr
50 55 60

Gln Gly Met His Glu Ile Ala Glu Ala Ile Arg Ala Val Ile Pro Pro
65 70 75 80

Thr Thr Ala Pro Val Pro Ser Gly Tyr Leu Ile Gln His Asp Glu Ala
85 90 95

Glu Glu Ile Pro Leu Gly Asp Leu Phe Lys Glu Gln Glu Glu Arg Ile
100 105 110

Val Ser Phe Gln Pro Asp Tyr Pro Ile Thr Ala Arg Ile His Ala His
115 120 125

Leu Lys Ala Tyr Ala Lys Ile Asn Glu Glu Ser Leu Asp Arg Ala Arg

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130 135 140

Arg Leu Leu Trp Trp His Tyr Asn Cys Leu Leu Trp Gly Glu Ala Thr
145 150 155 160

Val Thr Asn Tyr Ile Ser Arg Leu Arg Thr Trp Leu Ser Thr Pro Glu
165 170 175

Lys Tyr Arg Gly Arg Asp Ala Pro Thr Ile Glu Ala Ile Thr Arg Pro
180 185 190

Ile Gln Val Ala Gln Gly Gly Arg Lys Thr Ser Thr Ala Thr Arg Lys
195 200 205

Pro Arg Gly Leu Glu Pro Arg Arg Arg Lys Val Lys Thr Thr Val Val
210 215 220

Tyr Gly Arg Arg Arg Ser Lys Ser Arg Glu Arg Ala Ser Ser Pro
225 230 235 240

Gln Arg Ala Gly Ser Pro Leu Pro Arg Ser Ser Ser Ser His His Arg
245 250 255

Ser Pro Ser Pro Arg Lys
260

<210> 138
<211> 305
<212> PRT
<213> Duck hepatitis B virus

<400> 138
Met Trp Asp Leu Arg Leu His Pro Ser Pro Phe Gly Ala Ala Cys Gln
1 5 10 15

Gly Ile Phe Thr Ser Ser Leu Leu Leu Phe Leu Val Thr Val Pro Leu
20 25 30

Val Cys Thr Ile Val Tyr Asp Ser Cys Leu Cys Met Asp Ile Asn Ala
35 40 45

Ser Arg Ala Leu Ala Asn Val Tyr Asp Leu Pro Asp Asp Phe Phe Pro
50 55 60

Lys Ile Asp Asp Leu Val Arg Asp Ala Lys Asp Ala Leu Glu Pro Tyr
65 70 75 80

Trp Arg Asn Asp Ser Ile Lys Lys His Val Leu Ile Ala Thr His Phe
85 90 95

Val Asp Leu Ile Glu Asp Phe Trp Gln Thr Thr Gln Gly Met His Glu
100 105 110

Ile Ala Glu Ala Leu Arg Ala Ile Ile Pro Ala Thr Thr Ala Pro Val
115 120 125

Pro Gln Gly Phe Leu Val Gln His Glu Glu Ala Glu Glu Ile Pro Leu
130 135 140

Gly Glu Leu Phe Arg Tyr Gln Glu Glu Arg Leu Thr Asn Phe Gln Pro
145 150 155 160

Asp Tyr Pro Val Thr Ala Arg Ile His Ala His Leu Lys Ala Tyr Ala

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165 170 175

Lys Ile Asn Glu Ser Leu Asp Arg Ala Arg Arg Leu Leu Trp Trp
180 185 190

His Tyr Asn Cys Leu Leu Trp Gly Glu Pro Asn Val Thr Asn Tyr Ile
195 200 205

Ser Arg Leu Arg Thr Trp Leu Ser Thr Pro Glu Lys Tyr Arg Gly Lys
210 215 220

Asp Ala Pro Thr Ile Glu Ala Ile Thr Arg Pro Ile Gln Val Ala Gln
225 230 235 240

Gly Gly Arg Asn Lys Thr Gln Gly Val Arg Lys Ser Arg Gly Leu Glu
245 250 255

Pro Arg Arg Arg Val Lys Thr Thr Ile Val Tyr Gly Arg Arg Arg
260 265 270

Ser Lys Ser Arg Glu Arg Arg Ala Pro Thr Pro Gln Arg Ala Gly Ser
275 280 285

Pro Leu Pro Arg Thr Ser Arg Asp His His Arg Ser Pro Ser Pro Arg
290 295 300

Glu
305

<210> 139
<211> 212
<212> PRT
<213> Haemophilus influenzae

<400> 139
Met Lys Lys Thr Leu Leu Gly Ser Leu Ile Leu Leu Ala Phe Ala Gly
1 5 10 15

Asn Val Gln Ala Ala Ala Asn Ala Asp Thr Ser Gly Thr Val Thr Phe
20 25 30

Phe Gly Lys Val Val Glu Asn Thr Cys Gln Val Asn Gln Asp Ser Glu
35 40 45

Tyr Glu Cys Asn Leu Asn Asp Val Gly Lys Asn His Leu Ser Gln Gln
50 55 60

Gly Tyr Thr Ala Met Gln Thr Pro Phe Thr Ile Thr Leu Glu Asn Cys
65 70 75 80

Asn Val Thr Thr Thr Asn Asn Lys Pro Lys Ala Thr Lys Val Gly Val
85 90 95

Tyr Phe Tyr Ser Trp Glu Ile Ala Asp Lys Asp Asn Lys Tyr Thr Leu
100 105 110

Lys Asn Ile Lys Glu Asn Thr Gly Thr Asn Asp Ser Ala Asn Lys Val
115 120 125

Asn Ile Gln Leu Leu Glu Asp Asn Gly Thr Ala Glu Ile Lys Val Val
130 135 140

Gly Lys Thr Thr Thr Asp Phe Thr Ser Glu Asn His Asn Gly Ala Gly

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<210> 140
<211> 139
<212> PRT
<213> Pseudomonas stutzeri

<400> 140
Met Lys Ala Gln Met Gln Lys Gly Phe Thr Leu Ile Glu Leu Met Ile
  1             5             10             15

Val Val Ala Ile Ile Gly Ile Leu Ala Ala Ile Ala Leu Pro Ala Tyr
      20             25             30

Gln Asp Tyr Thr Val Arg Ser Asn Ala Ala Ala Ala Leu Ala Glu Ile
      35             40             45

Thr Pro Gly Lys Ile Gly Phe Glu Gln Ala Ile Asn Glu Gly Lys Thr
      50             55             60

Pro Ser Leu Thr Ser Thr Asp Glu Gly Tyr Ile Gly Ile Thr Asp Ser
      65             70             75             80

Thr Ser Tyr Cys Asp Val Asp Leu Asp Thr Ala Ala Asp Gly His Ile
      85             90             95

Glu Cys Thr Ala Lys Gly Gly Asn Ala Gly Lys Phe Asp Gly Lys Thr
      100            105            110

Ile Thr Leu Asn Arg Thr Ala Asp Gly Glu Trp Ser Cys Ala Ser Thr
      115            120            125

Leu Asp Ala Lys Tyr Lys Pro Gly Lys Cys Ser
      130            135

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<400> 141
Met Thr Lys Phe Val Thr Arg Phe Leu Lys Asp Glu Ser Gly Ala Thr
1 5 10 15
Ala Ile Glu Tyr 20 Gly Leu Ile Val 25 Ala Leu Ile Ala Val 30 Ile Val
Thr Ala Val Thr Thr Leu Gly Thr 40 Asn Leu Arg Thr Ala 45 Phe Thr Lys

Ala Gly Ala Ala Val Ser Thr Ala Ala Gly Thr
50 55

<210> 142
<211> 173
<212> PRT
<213> Escherichia coli

<400> 142
Met Ala Val Val Ser Phe Gly Val Asn Ala Ala Pro Thr Ile Pro Gln
1 5 10 15
Gly Gln Gly Lys Val Thr Phe Asn Gly Thr Val Val Asp Ala Pro Cys
20 25 30
Ser Ile Ser Gln Lys Ser Ala Asp Gln Ser Ile Asp Phe Gly Gln Leu
35 40 45
Ser Lys Ser Phe Leu Glu Ala Gly Gly Val Ser Lys Pro Met Asp Leu
50 55 60
Asp Ile Glu Leu Val Asn Cys Asp Ile Thr Ala Phe Lys Gly Gly Asn
65 70 75
Gly Ala Gln Lys Gly Thr Val Lys Leu Ala Phe Thr Gly Pro Ile Val
85 90 95
Asn Gly His Ser Asp Glu Leu Asp Thr Asn Gly Gly Thr Gly Thr Ala
100 105 110
Ile Val Val Gln Gly Ala Gly Lys Asn Val Val Phe Asp Gly Ser Glu
115 120 125
Gly Asp Ala Asn Thr Leu Lys Asp Gly Glu Asn Val Leu His Tyr Thr
130 135 140
Ala Val Val Lys Lys Ser Ser Ala Val Gly Ala Ala Val Thr Glu Gly
145 150 155 160
Ala Phe Ser Ala Val Ala Asn Phe Asn Leu Thr Tyr Gln
165 170

<210> 143
<211> 173
<212> PRT
<213> Escherichia coli

<400> 143
Met Ala Val Val Ser Phe Gly Val Asn Ala Ala Pro Thr Ile Pro Gln
1 5 10 15
Gly Gln Gly Lys Val Thr Phe Asn Gly Thr Val Val Asp Ala Pro Cys
20 25 30
Ser Ile Ser Gln Lys Ser Ala Asp Gln Ser Ile Asp Phe Gly Gln Leu
35 40 45
Ser Lys Ser Phe Leu Glu Ala Gly Gly Val Ser Lys Pro Met Asp Leu
50 55 60
Asp Ile Glu Leu Val Asn Cys Asp Ile Thr Ala Phe Lys Gly Gly Asn

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65 70 75 80
 Gly Ala Gln Lys Gly Thr Val Lys Leu Ala Phe Thr Gly Pro Ile Val
 85 90 95
 Asn Gly His Ser Asp Glu Leu Asp Thr Asn Gly Gly Thr Gly Thr Ala
 100 105 110
 Ile Val Val Gln Gly Ala Gly Lys Asn Val Val Phe Asp Gly Ser Glu
 115 120 125
 Gly Asp Ala Asn Thr Leu Lys Asp Gly Glu Asn Val Leu His Tyr Thr
 130 135 140
 Ala Val Val Lys Lys Ser Ser Ala Val Gly Ala Ala Val Thr Glu Gly
 145 150 155 160
 Ala Phe Ser Ala Val Ala Asn Phe Asn Leu Thr Tyr Gln
 165 170
 <210> 144
 <211> 172
 <212> PRT
 <213> Escherichia coli
 <400> 144
 Met Ala Val Val Ser Phe Gly Val Asn Ala Ala Pro Thr Thr Pro Gln
 1 5 10 15
 Gly Gln Gly Arg Val Thr Phe Asn Gly Thr Val Val Asp Ala Pro Cys
 20 25 30
 Ser Ile Ser Gln Lys Ser Ala Asp Gln Ser Ile Asp Phe Gly Gln Leu
 35 40 45
 Ser Lys Ser Phe Leu Ala Asn Asp Gly Gln Ser Lys Pro Met Asn Leu
 50 55 60
 Asp Ile Glu Leu Val Asn Cys Asp Ile Thr Ala Phe Lys Asn Gly Asn
 65 70 75 80
 Ala Lys Thr Gly Ser Val Lys Leu Ala Phe Thr Gly Pro Thr Val Ser
 85 90 95
 Gly His Pro Ser Glu Leu Ala Thr Asn Gly Gly Pro Gly Thr Ala Ile
 100 105 110
 Met Ile Gln Ala Ala Gly Lys Asn Val Pro Phe Asp Gly Thr Glu Gly
 115 120 125
 Asp Pro Asn Leu Leu Lys Asp Gly Asp Asn Val Leu His Tyr Thr Thr
 130 135 140
 Val Gly Lys Lys Ser Ser Asp Gly Asn Ala Gln Ile Thr Glu Gly Ala
 145 150 155 160
 Phe Ser Gly Val Ala Thr Phe Asn Leu Ser Tyr Gln
 165 170
 <210> 145
 <211> 853
 <212> DNA
 <213> Escherichia coli

10050898-011802

<220>
<221> CDS
<222> (281)..(829)

<400> 145
acgtttctgt ggctgcgagc atcttctctca ttcttctctc caaaaaccac ctcatgcaat 60
ataaacatct ataaataaag ataacaata gaatattaag ccaacaata aactgaaaaa 120
gtttgtccgc gatgctttac ctctatgagt caaaatggcc ccaatgttct atcttttggg 180
ggaaactgtg cagtgtttgc agtcaaaact gttgacaaac aaagtgtaca gaacgactgc 240
ccatgtcgat tttagaaatag ttttttgaaa ggaaagcagc atg aaa att aaa act 295
Met Lys Ile Lys Thr
1 5
ctg gca atc gtt gtt ctg tgc gct ctg tcc ctc agt tct acg acg gct 343
Leu Ala Ile Val Val Leu Ser Ala Leu Ser Leu Ser Ser Thr Thr Ala
10 15 20
ctg gcc gct gcc acg acg gtt aat ggt ggg acc gtt cac ttt aaa ggg 391
Leu Ala Ala Ala Thr Thr Val Asn Gly Gly Thr Val His Phe Lys Gly
25 30 35
gaa gtt gtt aac gcc gct tgc gca gtt gat gca ggc tct gtt gat caa 439
Glu Val Val Asn Ala Ala Cys Ala Val Asp Ala Gly Ser Val Asp Gln
40 45 50
acc gtt cag tta gga cag gtt cgt acc gca tgc ctg gca cag gaa gga 487
Thr Val Gln Leu Gly Gln Val Arg Thr Ala Ser Leu Ala Gln Glu Gly
55 60 65
gca acc agt tct gct gtc ggt ttt aac att cag ctg aat gat tgc gat 535
Ala Thr Ser Ser Ala Val Gly Phe Asn Ile Gln Leu Asn Asp Cys Asp
70 75 80 85
acc aat gtt gca tct aaa gcc gct gtt gcc ttt tta ggt acg gcg att 583
Thr Asn Val Ala Ser Lys Ala Ala Val Ala Phe Leu Gly Thr Ala Ile
90 95 100
gat gcg ggt cat acc aac gtt ctg gct ctg cag agt tca gct gcg ggt 631
Asp Ala Gly His Thr Asn Val Leu Ala Leu Gln Ser Ser Ala Ala Gly
105 110 115
agc gca aca aac gtt ggt gtg cag atc ctg gac aga acg ggt gct gcg 679
Ser Ala Thr Asn Val Gly Val Gln Ile Leu Asp Arg Thr Gly Ala Ala
120 125 130
ctg acg ctg gat ggt gcg aca ttt agt tca gaa aca acc ctg aat aac 727
Leu Thr Leu Asp Gly Ala Thr Phe Ser Ser Glu Thr Thr Leu Asn Asn
135 140 145
gga acc aat acc att ccg ttc cag gcg cgt tat ttt gca acc ggg gcc 775
Gly Thr Asn Thr Ile Pro Phe Gln Ala Arg Tyr Phe Ala Thr Gly Ala
150 155 160 165
gca acc ccg ggt gct gct aat gcg gat gcg acc ttc aag gtt cag tat 823
Ala Thr Pro Gly Ala Ala Asn Ala Asp Ala Thr Phe Lys Val Gln Tyr
170 175 180
caa taa cctacctagg ttcagggacg ttca 853
Gln

105033.011002

<210> 146
<211> 182
<212> PRT
<213> Escherichia coli

<400> 146
Met Lys Ile Lys Thr Leu Ala Ile Val Val Leu Ser Ala Leu Ser Leu
1 5 10 15
Ser Ser Thr Thr Ala Leu Ala Ala Thr Thr Val Asn Gly Gly Thr
20 25 30
Val His Phe Lys Gly Glu Val Val Asn Ala Ala Cys Ala Val Asp Ala
35 40 45
Gly Ser Val Asp Gln Thr Val Gln Leu Gly Gln Val Arg Thr Ala Ser
50 55 60
Leu Ala Gln Glu Gly Ala Thr Ser Ser Ala Val Gly Phe Asn Ile Gln
65 70 75
Leu Asn Asp Cys Asp Thr Asn Val Ala Ser Lys Ala Ala Val Ala Phe
85 90 95
Leu Gly Thr Ala Ile Asp Ala Gly His Thr Asn Val Leu Ala Leu Gln
100 105 110
Ser Ser Ala Ala Gly Ser Ala Thr Asn Val Gly Val Gln Ile Leu Asp
115 120 125
Arg Thr Gly Ala Ala Leu Thr Leu Asp Gly Ala Thr Phe Ser Ser Glu
130 135 140
Thr Thr Leu Asn Asn Gly Thr Asn Thr Ile Pro Phe Gln Ala Arg Tyr
145 150 155 160
Phe Ala Thr Gly Ala Ala Thr Pro Gly Ala Ala Asn Ala Asp Ala Thr
165 170 175
Phe Lys Val Gln Tyr Gln
180

<210> 147
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: FLAG peptide

<400> 147
Cys Gly Gly Asp Tyr Lys Asp Asp Asp Lys
1 5 10

<210> 148
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 148
ccggaattca tggacattga cccttataaa g

31

<210> 149
<211> 37
<212> DNA
<213> Artificial Sequence

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<220>
 <223> Description of Artificial Sequence: primer

<400> 149
 gtgcagtatg gtgaggtgag gaatgctcag gagactc 37

<210> 150
 <211> 37
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer

<400> 150
 gsgtctcctg agcattcctc acctcaccat actgcac 37

<210> 151
 <211> 33
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer

<400> 151
 cttccaaaag tgagggaaga aatgtgaaac cac 33

<210> 152
 <211> 47
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer

<400> 152
 cgcgtcccaa gcttctaaac aacagtagtc tccggaagcg ttgatag 47

<210> 153
 <211> 33
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer

<400> 153
 gtggtttcac atttcttccc tcaacttttg aag 33

<210> 154
 <211> 281
 <212> PRT
 <213> Saccharomyces cerevisiae

<400> 154
 Met Ser Glu Tyr Gln Pro Ser Leu Phe Ala Leu Asn Pro Met Gly Phe

105636.01502

1	5	10	15
Ser Pro Leu Asp Gly Ser Lys Ser Thr Asn Glu Asn Val Ser Ala Ser	20	25	30
Thr Ser Thr Ala Lys Pro Met Val Gly Gln Leu Ile Phe Asp Lys Phe	35	40	45
Ile Lys Thr Glu Glu Asp Pro Ile Ile Lys Gln Asp Thr Pro Ser Asn	50	55	60
Leu Asp Phe Asp Phe Ala Leu Pro Gln Thr Ala Thr Ala Pro Asp Ala	65	70	75
Lys Thr Val Leu Pro Ile Pro Glu Leu Asp Asp Ala Val Val Glu Ser	85	90	95
Phe Phe Ser Ser Ser Thr Asp Ser Thr Pro Met Phe Glu Tyr Glu Asn	100	105	110
Leu Glu Asp Asn Ser Lys Glu Trp Thr Ser Leu Phe Asp Asn Asp Ile	115	120	125
Pro Val Thr Thr Asp Asp Val Ser Leu Ala Asp Lys Ala Ile Glu Ser	130	135	140
Thr Glu Glu Val Ser Leu Val Pro Ser Asn Leu Glu Val Ser Thr Thr	145	150	155
Ser Phe Leu Pro Thr Pro Val Leu Glu Asp Ala Lys Leu Thr Thr Thr	165	170	175
Arg Lys Val Lys Lys Pro Asn Ser Val Val Lys Lys Ser His His Val	180	185	190
Gly Lys Asp Asp Glu Ser Arg Leu Asp His Leu Gly Val Val Ala Tyr	195	200	205
Asn Arg Lys Gln Arg Ser Ile Pro Leu Ser Pro Ile Val Pro Glu Ser	210	215	220
Ser Asp Pro Ala Ala Leu Lys Arg Ala Arg Asn Thr Glu Ala Ala Arg	225	230	235
Arg Ser Arg Ala Arg Lys Leu Gln Arg Met Lys Gln Leu Glu Asp Lys	245	250	255
Val Glu Glu Leu Leu Ser Lys Asn Tyr His Leu Glu Asn Glu Val Ala	260	265	270
Arg Leu Lys Lys Leu Val Gly Glu Arg	275	280	

<210> 155
 <211> 181
 <212> PRT
 <213> Escherichia coli

<400> 155
 Met Lys Ile Lys Thr Leu Ala Ile Val Val Leu Ser Ala Leu Ser Leu
 1 5 10
 Ser Ser Thr Ala Ala Leu Ala Ala Ala Thr Thr Val Asn Gly Gly Thr
 20 25 30

10050603.011002

Val His Phe Lys Gly Glu Val Val Asn Ala Ala Cys Ala Val Asp Ala
 35 40 45

Gly Ser Val Asp Gln Thr Val Gln Leu Gly Gln Val Arg Thr Ala Ser
 50 55 60

Leu Ala Gln Glu Gly Ala Thr Ser Ser Ala Val Gly Phe Asn Ile Gln
 65 70 75 80

Leu Asn Asp Cys Asp Thr Asn Val Ala Ser Lys Ala Ala Val Ala Phe
 85 90 95

Leu Gly Thr Ala Ile Asp Ala Gly His Thr Asn Val Leu Ala Leu Gln
 100 105 110

Ser Ser Ala Ala Gly Ser Ala Thr Asn Val Gly Val Gln Ile Leu Asp
 115 120 125

Arg Thr Gly Ala Ala Leu Thr Leu Asp Gly Ala Thr Phe Ser Ser Glu
 130 135 140

Thr Thr Leu Asn Asn Gly Thr Asn Thr Ile Pro Phe Gln Ala Arg Tyr
 145 150 155 160

Phe Ala Gly Ala Ala Thr Pro Gly Ala Ala Asn Ala Asp Ala Thr Phe
 165 170 175

Lys Val Gln Tyr Gln
 180

<210> 156
 <211> 447
 <212> DNA
 <213> Hepatitis B

<220>
 <221> CDS
 <222> (1)..(447)

<400> 156
 atg gac att gac cct tat aaa gaa ttt gga gct act gtg gag tta ctc 48
 Met Asp Ile Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu
 1 5 10 15

tcg ttt ttg cct tct gac ttc ttt cct tcc gta cga gat ctt cta gat 96
 Ser Phe Leu Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp
 20 25 30

acc gcc gca gct ctg tat cgg gat gcc tta gag tct cct gag cat tgt 144
 Thr Ala Ala Ala Leu Tyr Arg Asp Ala Leu Glu Ser Pro Glu His Cys
 35 40 45

tca cct cac cat act gca ctc agg caa gca att ctt tgc tgg gga gac 192
 Ser Pro His His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Asp
 50 55 60

tta atg act cta gct acc tgg gtg ggt act aat tta gaa gat cca gca 240
 Leu Met Thr Leu Ala Thr Trp Val Gly Thr Asn Leu Glu Asp Pro Ala
 65 70 75 80

tct agg gac cta gta gtc agt tat gtc aac act aat gtg ggc cta aag 288
 Ser Arg Asp Leu Val Val Ser Tyr Val Asn Thr Asn Val Gly Leu Lys

20050808-011502

	85		90		95	
ttc aga caa tta ttg tgg ttt cac att tct tgt ctc act ttt gga aga						336
Phe Arg Gln Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg						
	100		105		110	
gaa acg gtt cta gag tat ttg gtc tct ttt gga gtg tgg att cgc act						384
Glu Thr Val Leu Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr						
	115		120		125	
cct cca gcc tat aga cca cca aat gcc cct atc cta tca acg ctt ccg						432
Pro Pro Ala Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro						
	130		135		140	
gag act act gtt gtt						447
Glu Thr Thr Val Val						
145						
<210> 157						
<211> 149						
<212> PRT						
<213> Hepatitis B						
<400> 157						
Met Asp Ile Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu						
1	5		10		15	
Ser Phe Leu Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp						
20		25		30		
Thr Ala Ala Ala Leu Tyr Arg Asp Ala Leu Glu Ser Pro Glu His Cys						
35		40		45		
Ser Pro His His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Asp						
50		55		60		
Leu Met Thr Leu Ala Thr Trp Val Gly Thr Asn Leu Glu Asp Pro Ala						
65		70		75		80
Ser Arg Asp Leu Val Val Ser Tyr Val Asn Thr Asn Val Gly Leu Lys						
	85		90		95	
Phe Arg Gln Leu Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg						
100		105		110		
Glu Thr Val Leu Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr						
115		120		125		
Pro Pro Ala Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro						
130		135		140		
Glu Thr Thr Val Val						
145						

<210> 158
 <211> 152
 <212> PRT
 <213> Hepatitis B
 <400> 158

105088.011002

Met Asp Ile Asp Pro Tyr Lys Glu Phe Gly Ala Thr Val Glu Leu Leu
1 5 10 15

Ser Phe Leu Pro Ser Asp Phe Phe Pro Ser Val Arg Asp Leu Leu Asp
20 25 30

Thr Ala Ala Ala Leu Tyr Arg Asp Ala Leu Glu Ser Pro Glu His Cys
35 40 45

Ser Pro His His Thr Ala Leu Arg Gln Ala Ile Leu Cys Trp Gly Asp
50 55 60

Leu Met Thr Leu Ala Thr Trp Val Gly Thr Asn Leu Glu Asp Gly Gly
65 70 75 80

Lys Gly Gly Ser Arg Asp Leu Val Val Ser Tyr Val Asn Thr Asn Val
85 90 95

Gly Leu Lys Phe Arg Gln Leu Leu Trp Phe His Ile Ser Cys Leu Thr
100 105 110

Phe Gly Arg Glu Thr Val Leu Glu Tyr Leu Val Ser Phe Gly Val Trp
115 120 125

Ile Arg Thr Pro Pro Ala Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser
130 135 140

Thr Leu Pro Glu Thr Thr Val Val
145 150

<210> 159
<211> 132
<212> PRT
<213> Bacteriophage Q Beta

<400> 159
Ala Lys Leu Glu Thr Val Thr Leu Gly Asn Ile Gly Lys Asp Gly Lys
1 5 10 15

Gln Thr Leu Val Leu Asn Pro Arg Gly Val Asn Pro Thr Asn Gly Val
20 25 30

Ala Ser Leu Ser Gln Ala Gly Ala Val Pro Ala Leu Glu Lys Arg Val
35 40 45

Thr Val Ser Val Ser Gln Pro Ser Arg Asn Arg Lys Asn Tyr Lys Val
50 55 60

Gln Val Lys Ile Gln Asn Pro Thr Ala Cys Thr Ala Asn Gly Ser Cys
65 70 75 80

Asp Pro Ser Val Thr Arg Gln Ala Tyr Ala Asp Val Thr Phe Ser Phe
85 90 95

Thr Gln Tyr Ser Thr Asp Glu Glu Arg Ala Phe Val Arg Thr Glu Leu
100 105 110

Ala Ala Leu Leu Ala Ser Pro Leu Leu Ile Asp Ala Ile Asp Gln Leu
115 120 125

Asn Pro Ala Tyr
130

10050898.011802

<210> 160
<211> 129
<212> PRT
<213> Bacteriophage R 17

<400> 160

Ala Ser Asn Phe Thr Gln Phe Val Leu Val Asn Asp Gly Gly Thr Gly
1 5 10 15
Asn Val Thr Val Ala Pro Ser Asn Phe Ala Asn Gly Val Ala Glu Trp
20 25 30
Ile Ser Ser Asn Ser Arg Ser Gln Ala Tyr Lys Val Thr Cys Ser Val
35 40 45
Arg Gln Ser Ser Ala Gln Asn Arg Lys Tyr Thr Ile Lys Val Glu Val
50 55 60
Pro Lys Val Ala Thr Gln Thr Val Gly Gly Val Glu Leu Pro Val Ala
65 70 75 80
Ala Trp Arg Ser Tyr Leu Asn Met Glu Leu Thr Ile Pro Ile Phe Ala
85 90 95
Thr Asn Ser Asp Cys Glu Leu Ile Val Lys Ala Met Gln Gly Leu Leu
100 105 110
Lys Asp Gly Asn Pro Ile Pro Ser Ala Ile Ala Ala Asn Ser Gly Ile
115 120 125
Tyr

<210> 161
<211> 130
<212> PRT
<213> Bacteriophage fr

<400> 161

Met Ala Ser Asn Phe Glu Glu Phe Val Leu Val Asp Asn Gly Gly Thr
1 5 10 15
Gly Asp Val Lys Val Ala Pro Ser Asn Phe Ala Asn Gly Val Ala Glu
20 25 30
Trp Ile Ser Ser Asn Ser Arg Ser Gln Ala Tyr Lys Val Thr Cys Ser
35 40 45
Val Arg Gln Ser Ser Ala Asn Asn Arg Lys Tyr Thr Val Lys Val Glu
50 55 60
Val Pro Lys Val Ala Thr Gln Val Gln Gly Gly Val Glu Leu Pro Val
65 70 75 80
Ala Ala Trp Arg Ser Tyr Met Asn Met Glu Leu Thr Ile Pro Val Phe
85 90 95
Ala Thr Asn Asp Asp Cys Ala Leu Ile Val Lys Ala Leu Gln Gly Thr

10050000.011002

100 105 110
Phe Lys Thr Gly Asn Pro Ile Ala Thr Ala Ile Ala Ala Asn Ser Gly
115 120 125
Ile Tyr
130
<210> 162
<211> 130
<212> PRT
<213> Bacteriophage GA

<400> 162
Met Ala Thr Leu Arg Ser Phe Val Leu Val Asp Asn Gly Gly Thr Gly
1 5 10 15
Asn Val Thr Val Val Pro Val Ser Asn Ala Asn Gly Val Ala Glu Trp
20 25 30
Leu Ser Asn Asn Ser Arg Ser Gln Ala Tyr Arg Val Thr Ala Ser Tyr
35 40 45
Arg Ala Ser Gly Ala Asp Lys Arg Lys Tyr Ala Ile Lys Leu Glu Val
50 55 60
Pro Lys Ile Val Thr Gln Val Val Asn Gly Val Glu Leu Pro Gly Ser
65 70 75 80
Ala Trp Lys Ala Tyr Ala Ser Ile Asp Leu Thr Ile Pro Ile Phe Ala
85 90 95
Ala Thr Asp Asp Val Thr Val Ile Ser Lys Ser Leu Ala Gly Leu Phe
100 105 110
Lys Val Gly Asn Pro Ile Ala Glu Ala Ile Ser Ser Gln Ser Gly Phe
115 120 125
Tyr Ala
130

<210> 163
<211> 132
<212> PRT
<213> Bacteriophage SP

<400> 163
Met Ala Lys Leu Asn Gln Val Thr Leu Ser Lys Ile Gly Lys Asn Gly
1 5 10 15
Asp Gln Thr Leu Thr Leu Thr Pro Arg Gly Val Asn Pro Thr Asn Gly
20 25 30
Val Ala Ser Leu Ser Glu Ala Gly Ala Val Pro Ala Leu Glu Lys Arg
35 40 45
Val Thr Val Ser Val Ala Gln Pro Ser Arg Asn Arg Lys Asn Phe Lys
50 55 60

100503030.011002

Val Gln Ile Lys Leu Gln Asn Pro Thr Ala Cys Thr Arg Asp Ala Cys
65 70 75 80
Asp Pro Ser Val Thr Arg Ser Ala Phe Ala Asp Val Thr Leu Ser Phe
85 90 95
Thr Ser Tyr Ser Thr Asp Glu Glu Arg Ala Leu Ile Arg Thr Glu Leu
100 105 110
Ala Ala Leu Leu Ala Asp Pro Leu Ile Val Asp Ala Ile Asp Asn Leu
115 120 125
Asn Pro Ala Tyr
130

<210> 164
<211> 130
<212> PRT
<213> Bacteriophage MS2

<400> 164

Met Ala Ser Asn Phe Thr Gln Phe Val Leu Val Asp Asn Gly Gly Thr
1 5 10 15
Gly Asp Val Thr Val Ala Pro Ser Asn Phe Ala Asn Gly Val Ala Glu
20 25 30
Trp Ile Ser Ser Asn Ser Arg Ser Gln Ala Tyr Lys Val Thr Cys Ser
35 40 45
Val Arg Gln Ser Ser Ala Gln Asn Arg Lys Tyr Thr Ile Lys Val Glu
50 55 60
Val Pro Lys Val Ala Thr Gln Thr Val Gly Gly Val Glu Leu Pro Val
65 70 75 80
Ala Ala Trp Arg Ser Tyr Leu Asn Met Glu Leu Thr Ile Pro Ile Phe
85 90 95
Ala Thr Asn Ser Asp Cys Glu Leu Ile Val Lys Ala Met Gln Gly Leu
100 105 110
Leu Lys Asp Gly Asn Pro Ile Pro Ser Ala Ile Ala Asn Ser Gly
115 120 125
Ile Tyr
130

<210> 165
<211> 133
<212> PRT
<213> Bacteriophage M11

<400> 165
Met Ala Lys Leu Gln Ala Ile Thr Leu Ser Gly Ile Gly Lys Lys Gly
1 5 10 15
Asp Val Thr Leu Asp Leu Asn Pro Arg Gly Val Asn Pro Thr Asn Gly
20 25 30

10050608 011302

Val Ala Ala Leu Ser Glu Ala Gly Ala Val Pro Ala Leu Glu Lys Arg
35 40 45

Val Thr Ile Ser Val Ser Gln Pro Ser Arg Asn Arg Lys Asn Tyr Lys
50 55 60

Val Gln Val Lys Ile Gln Asn Pro Thr Ser Cys Thr Ala Ser Gly Thr
65 70 75 80

Cys Asp Pro Ser Val Thr Arg Ser Ala Tyr Ser Asp Val Thr Phe Ser
85 90 95

Phe Thr Gln Tyr Ser Thr Val Glu Glu Arg Ala Leu Val Arg Thr Glu
100 105 110

Leu Gln Ala Leu Leu Ala Asp Pro Met Leu Val Asn Ala Ile Asp Asn
115 120 125

Leu Asn Pro Ala Tyr
130

<210> 166

<211> 133

<212> PRT

<213> Bacteriophage MX1

<400> 166

Met Ala Lys Leu Gln Ala Ile Thr Leu Ser Gly Ile Gly Lys Asn Gly
1 5 10 15

Asp Val Thr Leu Asn Leu Asn Pro Arg Gly Val Asn Pro Thr Asn Gly
20 25 30

Val Ala Ala Leu Ser Glu Ala Gly Ala Val Pro Ala Leu Glu Lys Arg
35 40 45

Val Thr Ile Ser Val Ser Gln Pro Ser Arg Asn Arg Lys Asn Tyr Lys
50 55 60

Val Gln Val Lys Ile Gln Asn Pro Thr Ser Cys Thr Ala Ser Gly Thr
65 70 75 80

Cys Asp Pro Ser Val Thr Arg Ser Ala Tyr Ala Asp Val Thr Phe Ser
85 90 95

Phe Thr Gln Tyr Ser Thr Asp Glu Glu Arg Ala Leu Val Arg Thr Glu
100 105 110

Leu Lys Ala Leu Leu Ala Asp Pro Met Leu Ile Asp Ala Ile Asp Asn
115 120 125

Leu Asn Pro Ala Tyr
130

<210> 167

<211> 330

<212> PRT

<213> Bacteriophage NL95

<400> 167

10050898.011002

Met Ala Lys Leu Asn Lys Val Thr Leu Thr Gly Ile Gly Lys Ala Gly
1 5 10 15

Asn Gln Thr Leu Thr Leu Thr Pro Arg Gly Val Asn Pro Thr Asn Gly
20 25 30

Val Ala Ser Leu Ser Glu Ala Gly Ala Val Pro Ala Leu Glu Lys Arg
35 40 45

Val Thr Val Ser Val Ala Gln Pro Ser Arg Asn Arg Lys Asn Tyr Lys
50 55 60

Val Gln Ile Lys Leu Gln Asn Pro Thr Ala Cys Thr Lys Asp Ala Cys
65 70 75 80

Asp Pro Ser Val Thr Arg Ser Gly Ser Arg Asp Val Thr Leu Ser Phe
85 90 95

Thr Ser Tyr Ser Thr Glu Arg Glu Arg Ala Leu Ile Arg Thr Glu Leu
100 105 110

Ala Ala Leu Leu Lys Asp Asp Leu Ile Val Asp Ala Ile Asp Asn Leu
115 120 125

Asn Pro Ala Tyr Trp Ala Ala Leu Leu Ala Ala Ser Pro Gly Gly Gly
130 135 140

Asn Asn Pro Tyr Pro Gly Val Pro Asp Ser Pro Asn Val Lys Pro Pro
145 150 155 160

Gly Gly Thr Gly Thr Tyr Arg Cys Pro Phe Ala Cys Tyr Arg Arg Gly
165 170 175

Glu Leu Ile Thr Glu Ala Lys Asp Gly Ala Cys Ala Leu Tyr Ala Cys
180 185 190

Gly Ser Glu Ala Leu Val Glu Phe Glu Tyr Ala Leu Glu Asp Phe Leu
195 200 205

Gly Asn Glu Phe Trp Arg Asn Trp Asp Gly Arg Leu Ser Lys Tyr Asp
210 215 220

Ile Glu Thr His Arg Arg Cys Arg Gly Asn Gly Tyr Val Asp Leu Asp
225 230 235 240

Ala Ser Val Met Gln Ser Asp Glu Tyr Val Leu Ser Gly Ala Tyr Asp
245 250 255

Val Val Lys Met Gln Pro Pro Gly Thr Phe Asp Ser Pro Arg Tyr Tyr
260 265 270

Leu His Leu Met Asp Gly Ile Tyr Val Asp Leu Ala Glu Val Thr Ala
275 280 285

Tyr Arg Ser Tyr Gly Met Val Ile Gly Phe Trp Thr Asp Ser Lys Ser
290 295 300

Pro Gln Leu Pro Thr Asp Phe Thr Arg Phe Asn Arg His Asn Cys Pro
305 310 315 320

Val Gln Thr Val Ile Val Ile Pro Ser Leu
325 330

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<210> 168
 <211> 134
 <212> PRT
 <213> Apis mellifera

<400> 168
 Ile Ile Tyr Pro Gly Thr Leu Trp Cys Gly His Gly Asn Lys Ser Ser
 1 5 10 15
 Gly Pro Asn Glu Leu Gly Arg Phe Lys His Thr Asp Ala Cys Arg
 20 25 30
 Thr His Asp Met Cys Pro Asp Val Met Ser Ala Gly Glu Ser Lys His
 35 40 45
 Gly Leu Thr Asn Thr Ala Ser His Thr Arg Leu Ser Cys Asp Cys Asp
 50 55 60
 Asp Lys Phe Tyr Asp Cys Leu Lys Asn Ser Ala Asp Thr Ile Ser Ser
 65 70 75 80
 Tyr Phe Val Gly Lys Met Tyr Phe Asn Leu Ile Asp Thr Lys Cys Tyr
 85 90 95
 Lys Leu Glu His Pro Val Thr Gly Cys Gly Glu Arg Thr Glu Gly Arg
 100 105 110
 Cys Leu His Tyr Thr Val Asp Lys Ser Lys Pro Lys Val Tyr Gln Trp
 115 120 125
 Phe Asp Leu Arg Lys Tyr
 130

<210> 169
 <211> 129
 <212> PRT
 <213> Apis mellifera

<400> 169
 Ile Ile Tyr Pro Gly Thr Leu Trp Cys Gly His Gly Asn Lys Ser Ser
 1 5 10 15
 Gly Pro Asn Glu Leu Gly Arg Phe Lys His Thr Asp Ala Cys Arg
 20 25 30
 Thr His Asp Met Cys Pro Asn Val Met Ser Ala Gly Glu Ser Lys His
 35 40 45
 Gly Leu Thr Asp Thr Ala Ser Arg Leu Ser Cys Asn Asp Asn Asp Leu
 50 55 60
 Phe Tyr Lys Asp Ser Ala Asp Thr Ile Ser Ser Tyr Phe Val Gly Lys
 65 70 75 80
 Met Tyr Phe Asn Leu Ile Asn Thr Lys Cys Tyr Lys Leu Glu His Pro
 85 90 95
 Val Thr Gly Cys Gly Glu Arg Thr Glu Gly Arg Cys Leu His Tyr Thr
 100 105 110
 Val Asp Lys Ser Lys Pro Lys Val Tyr Gln Trp Phe Asp Leu Arg Lys
 115 120 125

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Tyr

<210> 170
<211> 134
<212> PRT
<213> Apis dorsata

<400> 170
Ile Ile Tyr Pro Gly Thr Leu Trp Cys Gly His Gly Asn Val Ser Ser
1 5 10 15
Ser Pro Asp Glu Leu Gly Arg Phe Lys His Thr Asp Ser Cys Cys Arg
20 25 30
Ser His Asp Met Cys Pro Asp Val Met Ser Ala Gly Glu Ser Lys His
35 40 45
Gly Leu Thr Asn Thr Ala Ser His Thr Arg Leu Ser Cys Asp Cys Asp
50 55 60
Asp Lys Phe Tyr Asp Cys Leu Lys Asn Ser Ser Asp Thr Ile Ser Ser
65 70 75 80
Tyr Phe Val Gly Glu Met Tyr Phe Asn Ile Leu Asp Thr Lys Cys Tyr
85 90 95
Lys Leu Glu His Pro Val Thr Gly Cys Gly Lys Arg Thr Glu Gly Arg
100 105 110
Cys Leu Asn Tyr Thr Val Asp Lys Ser Lys Pro Lys Val Tyr Gln Trp
115 120 125
Phe Asp Leu Arg Lys Tyr
130

<210> 171
<211> 134
<212> PRT
<213> Apis cerana

<400> 171
Ile Ile Tyr Pro Gly Thr Leu Trp Cys Gly His Gly Asn Val Ser Ser
1 5 10 15
Gly Pro Asn Glu Leu Gly Arg Phe Lys His Thr Asp Ala Cys Cys Arg
20 25 30
Thr His Asp Met Cys Pro Asp Val Met Ser Ala Gly Glu Ser Lys His
35 40 45
Gly Leu Thr Asn Thr Ala Ser His Thr Arg Leu Ser Cys Asp Cys Asp
50 55 60
Asp Thr Phe Tyr Asp Cys Leu Lys Asn Ser Gly Glu Lys Ile Ser Ser
65 70 75 80
Tyr Phe Val Gly Lys Met Tyr Phe Asn Leu Ile Asp Thr Lys Cys Tyr
85 90 95
Lys Leu Glu His Pro Val Thr Gly Cys Gly Glu Arg Thr Glu Gly Arg
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Cys Leu Arg Tyr Thr Val Asp Lys Ser Lys Pro Lys Val Tyr Gln Trp
115 120 125

Phe Asp Leu Arg Lys Tyr
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<210> 172
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<212> PRT
<213> *Bombus pennsylvanicus*

<400> 172

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Gly Thr Asn Glu Leu Gly Leu Trp Lys Glu Thr Asp Ala Cys Cys Arg
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Thr His Asp Met Cys Pro Asp Ile Ile Glu Ala His Gly Ser Lys His
35 40 45
Gly Leu Thr Asn Pro Ala Asp Tyr Thr Arg Leu Asn Cys Glu Cys Asp
50 55 60
Glu Glu Phe Arg His Cys Leu His Asn Ser Gly Asp Ala Val Ser Ala
65 70 75 80
Ala Phe Val Gly Arg Thr Tyr Phe Thr Ile Leu Gly Thr Gln Cys Phe
85 90 95
Arg Leu Asp Tyr Pro Ile Val Lys Cys Lys Val Lys Ser Thr Ile Leu
100 105 110
Arg Glu Cys Lys Glu Tyr Glu Phe Asp Thr Asn Ala Pro Gln Lys Tyr
115 120 125
Gln Trp Phe Asp Val Leu Ser Tyr
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<210> 173
<211> 142
<212> PRT
<213> *Heloderma suspectum*

<400> 173
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Ala Ser Asp Tyr Ser Gln Leu Gly Thr Glu Lys Asp Thr Asp Met Cys
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Cys Arg Asp His Asp His Cys Ser Asp Thr Met Ala Ala Leu Glu Tyr
35 40 45
Lys His Gly Met Arg Asn Tyr Arg Pro His Thr Val Ser His Cys Asp
50 55 60
Cys Asp Asn Gln Phe Arg Ser Cys Leu Met Asn Val Lys Asp Arg Thr
65 70 75 80

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Ala Asp Leu Val Gly Met Thr Tyr Phe Thr Val Leu Lys Ile Ser Cys
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Phe Glu Leu Glu Glu Gly Glu Gly Cys Val Asp Asn Asn Phe Ser Gln
100 105 110

Gln Cys Thr Lys Ser Glu Ile Met Pro Val Ala Lys Leu Val Ser Ala
115 120 125

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<213> Heloderma suspectum

<400> 174

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Cys Arg Asp His Asp His Cys Glu Asn Trp Ile Ser Ala Leu Glu Tyr
35 40 45

Lys His Gly Met Arg Asn Tyr Tyr Pro Ser Thr Ile Ser His Cys Asp
50 55 60

Cys Asp Asn Gln Phe Arg Ser Cys Leu Met Lys Leu Lys Asp Gly Thr
65 70 75 80

Ala Asp Tyr Val Gly Gln Thr Tyr Phe Asn Val Leu Lys Ile Pro Cys
85 90 95

Phe Glu Leu Glu Glu Gly Glu Gly Cys Val Asp Trp Asn Phe Trp Leu
100 105 110

Glu Cys Thr Glu Ser Lys Ile Met Pro Val Ala Lys Leu Val Ser Ala
115 120 125

Ala Pro Tyr Gln Ala Gln Ala Glu Thr Gln Ser Gly Glu Gly Arg
130 135 140

<210> 175

<211> 142

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<213> Heloderma suspectum

<400> 175

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35 40 45

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Lys His Gly Met Arg Asn Tyr Tyr Pro Ser Thr Ile Ser His Cys Asp
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Cys Asp Asn Gln Phe Arg Ser Cys Leu Met Lys Leu Lys Asp Gly Thr
65 70 75 80

Ala Asp Tyr Val Gly Gln Thr Tyr Phe Asn Val Leu Lys Ile Pro Cys
85 90 95

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100 105 110

Glu Cys Thr Glu Ser Lys Ile Met Pro Val Ala Lys Leu Val Ser Ala
115 120 125

Ala Pro Tyr Gln Ala Gln Ala Glu Thr Gln Ser Gly Glu Gly
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<211> 574

<212> PRT

<213> IgE heavy chain

<400> 176

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35 40 45

Asp Ser Tyr Ile His Trp Ile Arg Gln Ala Pro Gly His Gly Leu Glu
50 55 60

Trp Val Gly Trp Ile Asn Pro Asn Ser Gly Gly Thr Asn Tyr Ala Pro
65 70 75 80

Arg Phe Gln Gly Arg Val Thr Met Thr Arg Asp Ala Ser Phe Ser Thr
85 90 95

Ala Tyr Met Asp Leu Arg Ser Leu Arg Ser Asp Asp Ser Ala Val Phe
100 105 110

Tyr Cys Ala Lys Ser Asp Pro Phe Trp Ser Asp Tyr Tyr Asn Phe Asp
115 120 125

Tyr Ser Tyr Thr Leu Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val
130 135 140

Ser Ser Ala Ser Thr Gln Ser Pro Ser Val Phe Pro Leu Thr Arg Cys
145 150 155 160

Cys Lys Asn Ile Pro Ser Asn Ala Thr Ser Val Thr Leu Gly Cys Leu
165 170 175

Ala Thr Gly Tyr Phe Pro Glu Pro Val Met Val Thr Trp Asp Thr Gly
180 185 190

Ser Leu Asn Gly Thr Thr Met Thr Leu Pro Ala Thr Thr Leu Thr Leu

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Gln	Ser	Glu	Leu	Thr	Leu	Ser	Gln	Lys	His	Trp	Leu	Ser	Asp	Arg	Thr
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Cys	Leu	Val	Val	Asp	Leu	Ala	Pro	Ser	Lys	Gly	Thr	Val	Asn	Leu	Thr
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Pro	Gly	Ser	Arg	Asp	Lys	Arg	Thr	Leu	Ala	Cys	Leu	Ile	Gln	Asn	Phe
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Met	Pro	Glu	Asp	Ile	Ser	Val	Gln	Trp	Leu	His	Asn	Glu	Val	Gln	Leu
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Pro	Asp	Ala	Arg	His	Ser	Thr	Gln	Pro	Arg	Lys	Thr	Lys	Gly	Ser	
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Gly	Phe	Phe	Val	Phe	Ser	Arg	Leu	Glu	Val	Thr	Arg	Ala	Glu	Trp	Glu

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 565 570

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Val Asn Leu Thr Trp Ser Arg Ala Ser Gly
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<210> 183
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1 5 10

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1 5 10

<210> 186
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1 5 10

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Val Lys Leu Pro Trp Arg Phe Tyr Gln Val
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<400> 189
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<210> 190
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<400> 190
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<210> 191
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<210> 192
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<210> 193
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<210> 195
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<210> 196
<211> 56
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<213> Oligonucleotide Primer

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<210> 197
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<212> DNA
<213> Oligonucleotide Primer

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<210> 207
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 <212> PRT
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<400> 207
 Cys Gly Gly Val Asn Leu Thr Trp Ser Arg Ala Ser Gly
 1 5 10

<210> 208
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 <212> PRT
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<400> 208
 Cys Gly Gly Val Asn Leu Pro Trp Ser Phe Gly Leu Glu
 1 5 10

<210> 209
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 <212> PRT
 <213> Bee venom phospholipase A2 cloning vector

<400> 209
 Ala Ala Ala Ser Gly Gly Cys Gly Gly
 1 5

<210> 210
 <211> 145
 <212> PRT
 <213> PLA₂ fusion protein

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 Met Ala Ile Ile Tyr Pro Gly Thr Leu Trp Cys Gly His Gly Asn Lys
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Ser Ser Gly Pro Asn Glu Leu Gly Arg Phe Lys His Thr Asp Ala Cys
 20 25 30

Cys Arg Thr Gln Asp Met Cys Pro Asp Val Met Ser Ala Gly Glu Ser
 35 40 45

Lys His Gly Leu Thr Asn Thr Ala Ser His Thr Arg Leu Ser Cys Asp
 50 55 60

Cys Asp Asp Lys Phe Tyr Asp Cys Leu Lys Asn Ser Ala Asp Thr Ile
 65 70 75 80

Ser Ser Tyr Phe Val Gly Lys Met Tyr Phe Asn Leu Ile Asp Thr Lys
 85 90 95

Cys Tyr Lys Leu Glu His Pro Val Thr Gly Cys Gly Glu Arg Thr Glu
 100 105 110

Gly Arg Cys Leu His Tyr Thr Val Asp Lys Ser Lys Pro Lys Val Tyr

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115 120 125
Gln Trp Phe Asp Leu Arg Lys Tyr Ala Ala Ala Ser Gly Gly Cys Gly
130 135 140

Gly
145

<210> 211
<211> 17
<212> PRT
<213> Ce4mimotope

<400> 211
Gly Glu Phe Cys Ile Asn His Arg Gly Tyr Trp Val Cys Gly Asp Pro
1 5 10 15

Ala

<210> 212
<211> 27
<212> PRT
<213> Synthetic M2 Peptide

<400> 212
Ser Leu Leu Thr Glu Val Glu Thr Pro Ile Arg Asn Glu Trp Gly Cys
1 5 10 15

Arg Cys Asn Gly Ser Ser Asp Gly Gly Gly Cys
20 25

<210> 213
<211> 97
<212> PRT
<213> Matrix protein M2

<400> 213
Met Ser Leu Leu Thr Glu Val Glu Thr Pro Ile Arg Asn Glu Trp Gly
1 5 10 15

Cys Arg Cys Asn Gly Ser Ser Asp Pro Leu Ala Ile Ala Ala Asn Ile
20 25 30

Ile Gly Ile Leu His Leu Ile Leu Trp Ile Leu Asp Arg Leu Phe Phe
35 40 45

Lys Cys Ile Tyr Arg Arg Phe Lys Tyr Gly Leu Lys Gly Gly Pro Ser
50 55 60

Thr Glu Gly Val Pro Lys Ser Met Arg Glu Glu Tyr Arg Lys Glu Gln
65 70 75 80

Gln Ser Ala Val Asp Ala Asp Asp Gly His Phe Val Ser Ile Glu Leu
85 90 95

Glu

<210> 214

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<211> 42
<212> DNA
<213> Oligonucleotide

<400> 214
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42

<210> 215
<211> 129
<212> PRT
<213> Bacteriophage f2

<400> 215
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1 5 10 15
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20 25 30
Ile Ser Ser Asn Ser Arg Ser Gln Ala Tyr Lys Val Thr Cys Ser Val
35 40 45
Arg Gln Ser Ser Ala Gln Asn Arg Lys Tyr Thr Ile Lys Val Glu Val
50 55 60
Pro Lys Val Ala Thr Gln Thr Val Gly Gly Val Glu Leu Pro Val Ala
65 70 75 80
Ala Trp Arg Ser Tyr Leu Asn Leu Glu Leu Thr Ile Pro Ile Phe Ala
85 90 95
Thr Asn Ser Asp Cys Glu Leu Ile Val Lys Ala Met Gln Gly Leu Leu
100 105 110
Lys Asp Gly Asn Pro Ile Pro Ser Ala Ile Ala Ala Asn Ser Gly Ile
115 120 125

Tyr

<210> 216
<211> 17
<212> PRT
<213> Circular Mimotope

<400> 216
Gly Glu Phe Cys Ile Asn His Arg Gly Tyr Trp Val Cys Gly Asp Pro

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1 5 10 15

Ala

<210> 217

<211> 329

<212> PRT

<213> Bacteriophage Q-beta

<400> 217

Met Ala Lys Leu Glu Thr Val Thr Leu Gly Asn Ile Gly Lys Asp Gly
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20 25 30

Val Ala Ser Leu Ser Gln Ala Gly Ala Val Pro Ala Leu Glu Lys Arg
35 40 45

Val Thr Val Ser Val Ser Gln Pro Ser Arg Asn Arg Lys Asn Tyr Lys
50 55 60

Val Gln Val Lys Ile Gln Asn Pro Thr Ala Cys Thr Ala Asn Gly Ser
65 70 75 80

Cys Asp Pro Ser Val Thr Arg Gln Ala Tyr Ala Asp Val Thr Phe Ser
85 90 95

Phe Thr Gln Tyr Ser Thr Asp Glu Glu Arg Ala Phe Val Arg Thr Glu
100 105 110

Leu Ala Ala Leu Leu Ala Ser Pro Leu Leu Ile Asp Ala Ile Asp Gln
115 120 125

Leu Asn Pro Ala Tyr Trp Thr Leu Leu Ile Ala Gly Gly Ser Gly
130 135 140

Ser Lys Pro Asp Pro Val Ile Pro Asp Pro Pro Ile Asp Pro Pro Pro
145 150 155 160

Gly Thr Gly Lys Tyr Thr Cys Pro Phe Ala Ile Trp Ser Leu Glu Gly
165 170 175

Val Tyr Glu Pro Pro Thr Lys Asn Arg Pro Trp Pro Ile Tyr Asn Ala
180 185 190

Val Glu Leu Gln Pro Arg Glu Phe Asp Val Ala Leu Lys Asp Leu Leu
195 200 205

Gly Asn Thr Lys Trp Arg Asp Trp Asp Ser Arg Leu Ser Tyr Thr Thr
210 215 220

Phe Arg Gly Cys Arg Gly Asn Gly Tyr Ile Asp Leu Asp Ala Thr Tyr
225 230 235 240

Leu Ala Thr Asp Gln Ala Met Arg Asp Gln Lys Tyr Asp Ile Arg Glu

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245 250 255

Gly Lys Lys Pro Gly Ala Phe Gly Asn Ile Glu Arg Phe Ile Tyr Leu
260 265 270

Lys Ser Ile Asn Ala Tyr Cys Ser Leu Ser Asp Ile Ala Ala Tyr His
275 280 285

Ala Asp Gly Val Ile Val Gly Phe Trp Arg Asp Pro Ser Ser Gly Gly
290 295 300

Ala Ile Pro Phe Asp Phe Thr Lys Phe Asp Lys Thr Lys Cys Pro Ile
305 310 315 320

Gln Ala Val Ile Val Val Pro Arg Ala
325

<210> 218

<211> 770

<212> PRT

<213> Amyloid-Beta Protein (Homo Sapiens)

<400> 218

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Ala Leu Glu Val Pro Thr Asp Gly Asn Ala Gly Leu Leu Ala Glu Pro
20 25 30

Gln Ile Ala Met Phe Cys Gly Arg Leu Asn Met His Met Asn Val Gln
35 40 45

Asn Gly Lys Trp Asp Ser Asp Pro Ser Gly Thr Lys Thr Cys Ile Asp
50 55 60

Thr Lys Glu Gly Ile Leu Gln Tyr Cys Gln Glu Val Tyr Pro Glu Leu
65 70 75 80

Gln Ile Thr Asn Val Val Glu Ala Asn Gln Pro Val Thr Ile Gln Asn
85 90 95

Trp Cys Lys Arg Gly Arg Lys Gln Cys Lys Thr His Pro His Phe Val
100 105 110

Ile Pro Tyr Arg Cys Leu Val Gly Glu Phe Val Ser Asp Ala Leu Leu
115 120 125

Val Pro Asp Lys Cys Lys Phe Leu His Gln Glu Arg Met Asp Val Cys
130 135 140

Glu Thr His Leu His Trp His Thr Val Ala Lys Glu Thr Cys Ser Glu
145 150 155 160

Lys Ser Thr Asn Leu His Asp Tyr Gly Met Leu Leu Pro Cys Gly Ile
165 170 175

Asp Lys Phe Arg Gly Val Glu Phe Val Cys Cys Pro Leu Ala Glu Glu

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180										185										190													
Ser	Asp	Asn	Val	Asp	Ser	Ala	Asp	Ala	Glu	Glu	Asp	Asp	Ser	Asp	Val	Ser	Asp	Val	Asp	Ser	Ala	Asp	Ala	Glu	Glu	Asp	Asp	Ser	Asp	Val	Ser	Asp	Val
		195						200																									
Trp	Trp	Gly	Gly	Ala	Asp	Thr	Asp	Tyr	Ala	Asp	Gly	Ser	Glu	Asp	Lys	Trp	Trp	Gly	Gly	Ala	Asp	Thr	Asp	Tyr	Ala	Asp	Gly	Ser	Glu	Asp	Lys		
		210						215																									
Val	Val	Glu	Val	Ala	Glu	Glu	Glu	Val	Ala	Glu	Val	Glu	Glu	Glu	240	Val	Val	Glu	Val	Ala	Glu	Glu	Glu	Val	Ala	Glu	Val	Glu	Glu	Glu	240		
		225						230																									
Glu	Ala	Asp	Asp	Asp	Glu	Asp	Asp	Glu	Asp	Gly	Asp	Glu	Val	Glu	Glu	255	Glu	Ala	Asp	Asp	Asp	Glu	Asp	Asp	Glu	Asp	Gly	Asp	Glu	Val	Glu	Glu	255
Glu	Ala	Glu	Glu	Pro	Tyr	Glu	Glu	Ala	Thr	Glu	Arg	Thr	Thr	Ser	Ile	270	Glu	Ala	Glu	Glu	Pro	Tyr	Glu	Glu	Ala	Thr	Glu	Arg	Thr	Thr	Ser	Ile	270
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Ser	Arg	Trp	Tyr	Phe	Asp	Val	Thr	Glu	Gly	Lys	Cys	Ala	Pro	Phe	Phe	320	Ser	Arg	Trp	Tyr	Phe	Asp	Val	Thr	Glu	Gly	Lys	Cys	Ala	Pro	Phe	Phe	320
Tyr	Gly	Gly	Cys	Gly	Gly	Asn	Arg	Asn	Phe	Asp	Thr	Glu	Gly	Tyr	335	Tyr	Gly	Gly	Cys	Gly	Gly	Asn	Arg	Asn	Phe	Asp	Thr	Glu	Gly	Tyr	335		
Cys	Met	Ala	Val	Cys	Gly	Ser	Ala	Met	Ser	Gln	Ser	Leu	Leu	Lys	Thr	350	Cys	Met	Ala	Val	Cys	Gly	Ser	Ala	Met	Ser	Gln	Ser	Leu	Leu	Lys	Thr	350
Thr	Gln	Glu	Pro	Leu	Ala	Arg	Asp	Pro	Val	Lys	Leu	Pro	Thr	Thr	Ala	365	Thr	Gln	Glu	Pro	Leu	Ala	Arg	Asp	Pro	Val	Lys	Leu	Pro	Thr	Thr	Ala	365
Ala	Ser	Thr	Pro	Asp	Ala	Val	Asp	Lys	Tyr	Leu	Glu	Thr	Pro	Gly	Asp	380	Ala	Ser	Thr	Pro	Asp	Ala	Val	Asp	Lys	Tyr	Leu	Glu	Thr	Pro	Gly	Asp	380
Glu	Asn	Glu	His	Ala	His	Phe	Gln	Lys	Ala	Lys	Glu	Arg	Leu	Glu	Ala	400	Glu	Asn	Glu	His	Ala	His	Phe	Gln	Lys	Ala	Lys	Glu	Arg	Leu	Glu	Ala	400
Lys	His	Arg	Glu	Arg	Met	Ser	Gln	Val	Met	Arg	Glu	Trp	Glu	Glu	Ala	415	Lys	His	Arg	Glu	Arg	Met	Ser	Gln	Val	Met	Arg	Glu	Trp	Glu	Glu	Ala	415
Glu	Arg	Gln	Ala	Lys	Asn	Leu	Pro	Lys	Ala	Asp	Lys	Lys	Ala	Val	Ile	430	Glu	Arg	Gln	Ala	Lys	Asn	Leu	Pro	Lys	Ala	Asp	Lys	Lys	Ala	Val	Ile	430
Gln	His	Phe	Gln	Glu	Lys	Val	Glu	Ser	Leu	Glu	Gln	Glu	Ala	Ala	Asn	445	Gln	His	Phe	Gln	Glu	Lys	Val	Glu	Ser	Leu	Glu	Gln	Glu	Ala	Ala	Asn	445
Glu	Arg	Gln	Gln	Leu	Val	Glu	Thr	His	Met	Ala	Arg	Val	Glu	Ala	Met	450	Glu	Arg	Gln	Gln	Leu	Val	Glu	Thr	His	Met	Ala	Arg	Val	Glu	Ala	Met	450
Leu	Asn	Asp	Arg	Arg	Arg	Leu	Ala	Leu	Glu	Asn	Tyr	Ile	Thr	Ala	Leu	480	Leu	Asn	Asp	Arg	Arg	Arg	Leu	Ala	Leu	Glu	Asn	Tyr	Ile	Thr	Ala	Leu	480
Gln	Ala	Val	Pro	Pro	Arg	Pro	Arg	His	Val	Phe	Asn	Met	Leu	Lys	Lys	495	Gln	Ala	Val	Pro	Pro	Arg	Pro	Arg	His	Val	Phe	Asn	Met	Leu	Lys	Lys	495
Tyr	Val	Arg	Ala	Glu	Gln	Lys	Asp	Arg	Gln	His	Thr	Leu	Lys	His	Phe	510	Tyr	Val	Arg	Ala	Glu	Gln	Lys	Asp	Arg	Gln	His	Thr	Leu	Lys	His	Phe	510
Glu	His	Val	Arg	Met	Val	Asp	Pro	Lys	Lys	Ala	Ala	Gln	Ile	Arg	Ser		Glu	His	Val	Arg	Met	Val	Asp	Pro	Lys	Lys	Ala	Ala	Gln	Ile	Arg	Ser	

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515 520 525

Gln Val Met Thr His Leu Arg Val Ile Tyr Glu Arg Met Asn Gln Ser
530 535 540

Leu Ser Leu Leu Tyr Asn Val Pro Ala Val Ala Glu Glu Ile Gln Asp
545 550 555

Glu Val Asp Glu Leu Leu Gln Lys Glu Gln Asn Tyr Ser Asp Asp Val
565 570 575

Leu Ala Asn Met Ile Ser Glu Pro Arg Ile Ser Tyr Gly Asn Asp Ala
580 585 590

Leu Met Pro Ser Leu Thr Glu Thr Lys Thr Thr Val Glu Leu Leu Pro
595 600 605

Val Asn Gly Glu Phe Ser Leu Asp Asp Leu Gln Pro Trp His Ser Phe
610 615 620

Gly Ala Asp Ser Val Pro Ala Asn Thr Glu Asn Glu Val Glu Pro Val
625 630 635

Asp Ala Arg Pro Ala Ala Asp Arg Gly Leu Thr Thr Arg Pro Gly Ser
645 650 655

Gly Leu Thr Asn Ile Lys Thr Glu Glu Ile Ser Glu Val Lys Met Asp
660 665 670

Ala Glu Phe Arg His Asp Ser Gly Tyr Glu Val His His Gln Lys Leu
675 680 685

Val Phe Phe Ala Glu Asp Val Gly Ser Asn Lys Gly Ala Ile Ile Gly
690 695 700

Leu Met Val Gly Gly Val Val Ile Ala Thr Val Ile Val Ile Thr Leu
705 710 715

Val Met Leu Lys Lys Lys Gln Tyr Thr Ser Ile His His Gly Val Val
725 730 735

Glu Val Asp Ala Ala Val Thr Pro Glu Glu Arg His Leu Ser Lys Met
740 745 750

Gln Gln Asn Gly Tyr Glu Asn Pro Thr Tyr Lys Phe Phe Glu Gln Met
755 760 765

Gln Asn
770

<210> 219

<211> 82

<212> PRT

<213> Beta-Amyloid Peptide Precursor (Homo Sapiens)

<400> 219

Gly Ser Gly Leu Thr Asn Ile Lys Thr Glu Glu Ile Ser Glu Val Lys

10050608.011802

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1           5           10           15
Met Asp Ala Glu Phe Arg His Asp Ser Gly Tyr Glu Val His His Gln
                20                25                30
Lys Leu Val Phe Phe Ala Glu Asp Val Gly Ser Asn Lys Gly Ala Ile
                35                40                45
Ile Gly Leu Met Val Gly Gly Val Val Ile Ala Thr Val Ile Ile Ile
                50                55                60
Thr Leu Val Met Leu Lys Lys Gln Tyr Thr Ser Asn His His Gly Val
                65                70                75                80
Val Glu

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<210> 220

<211> 42

<212> PRT

<213> Amyloid Beta Peptide

<400> 220

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Asp Ala Glu Phe Arg His Asp Ser Gly Tyr Glu Val His His Gln Lys
1           5           10           15
Leu Val Phe Phe Ala Glu Asp Val Gly Ser Asn Lys Gly Ala Ile Ile
                20                25                30
Gly Leu Met Val Gly Gly Val Val Ile Ala
                35                40

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221:

RANKL_human: TrEMBL:O14788: extracellular domain

YFRAQMDPNRIS EDGTHCIYRI LRLHENADFQ DTTLESQDTK LIPDSCRRIK QAFQGA VQKE
 LQHIVGSQHI RAEKAMVDGS WLDLAKRSKL EAQPPAHLTI NATDIPSGSH KVSLSWYHD
 RGWAKISNMT FSNGLIVNQ DGFYLYANI CFRHHETSGD LATEYLQLMV YVTKTSIKIP
 SSTLMKGG S TKYWSGNSEF HFYSINVGGF FKLRSGEEIS IEVSNP SLLD PDQDATYFGA FKVRDID

222:

RANKL_human: spliced isoform TrEMBL:O14788

MDPNRISE DG THCIYRILRL HENADFQDTT LESQDTKLIP DSCRRIKQAF QGAVQKELQH
 IVGSQHIRAE KAMVDGSWLD LAKRSKLEAQ PFAHLTINAT DIPSGSHKVS LSSWYHDRGW
 AKISNMTFSN GKLIVNQDGF YYLIANICFR HHETSGDLAT EYLQLMVYVT KTSIKIPSSH
 TLMKGGSTKY WSGNSEFHFY SINVGFFPKL RSGEEISIEV SNP SLLDPDQ DATYFGAFKV
 RDID

223:

RANKL_mouse: TrEMBL:O35235: extracellular domain

1050000.01002

YFRAQMDPNRI SEDSTHCFYR ILRLHENAGL QDSTLESED LPSDCRMKQ AFQGAQKEL
QHIVGQRFQ GAPAMMEGSW LDVAQRGKPE AQPFahlTIN AASIPSGSHK VTLSSWYHDR
GWAKISNMTL SNGKLRVNQD GFYYLYANIC FRHHETSGSV PTDYQLQMLVY VVKTSIKIPS
SHNLKMGST KNWSGNSEPH FYSINVGFF KLRAGEEISI QVSNPSLLDP DQDATYFGAF KVQDID

224:

RANKL_mouse spliced isoforms: TrEMBL:Q9JJK8

MKQAPQGA VQ KELQHVGPQ RFSGAPAMME GSWLDVAQRG KPEAQPFahl TINAASIPSG
SHKVTLSWY HDRGWAKISN MTLNKGKLRV NQDGFYYLYA NICFRHETS GSVPTDYQLQ
MVYVVKTSIK IPSSHNLKMG GSTRNWSGNS EFHFYSINVG GFFKL RAGEE ISIQVSNPSL
LDPDQDATYF GAFKVQDID

225:

MIF_rat: SwissProt

PMFIVNTNVP RASVPEGFLS ELTQQLAQAT GKPAQYIAVH VVPDQLMTFS GTSDPCALCS
LHSIGKIGGA QNRNYSKLLC GLLSDRLHIS PDRVYINYD MNAANVGWNG STFA

226:

MIF_mouse: SwissProt

PMFIVNTNVP RASVPEGFLS ELTQQLAQAT GKPAQYIAVH VVPDQLMTFS GTNDPCALCS
LHSIGKIGGA QNRNYSKLLC GLLSDRLHIS PDRVYINYD MNAANVGWNG STFA

227:

MIF_human: SwissProt

PMFIVNTNVP RASVDPGFLS ELTQQLAQAT GKPFQYIAVH VVPDQLMAFG GSSEPCALCS
LHSIGKIGGA QNRSYSKLLC GLLAERLRIS PDRVYINYD MNAANVGWNN STFA

228:

Human IL-17

ACCESSION #: AAC50341

1 mtpgktslvs lllllsleai vkagitiprn pgcpnsedkn fprtvmvnlh ihrntntnp
61 krssdyynrs tspwnlhrne dperypsvi eakcrhlgi nadgnvdyhm nsvpiqqeil
121 vlrrpphpcp nsfrlekilv svgtctvtpi vhhva

229:

Mouse IL-17

ACCESSION #: AAA37490

1 mspgrassvs lmlllllsla atvkaaaip qssacpntea kdfqmvkvn lkvfnslgak
61 vssrrpsdyl nrstspwtlh rnedpdryps viweaqcrhq rcvnaegkld hhmnsvliqq
121 eilvlkrepe scptfirvek mlvgvgctcv asivrgaa

230:

Human IL-13 (precursor)

105505505-01162

MALLTTVIALTCLGGFASPGVPVPSTALRELIEELVNITQNQKAPLCNGSMVWSINLTAGMYCAALESLINVSG
CSAIEKTQRMLSGFCPHKVSAGQFSSLHVRDTKIEVAQFVKDLLHLKKLFREGRFN

231:

Human IL-13 (processed)

GPVPPSTALR ELIEELVNIT QNQKAPLCNG SMVWSINLTA
GMYCAALES INVSGCSAIE KTQRMLSGFC PHKVSAGQFS SLHVRDTKIE VAQFVKDLLL
HLKKLFREGR FN

232:

Mouse IL-13 (processed)

GPVPRSVSLPLTLKELIEELSNITQDQTPCLNGSMVWSVDLAAGGFCVALDSLNISSNCNAIYRTQRILHGLCNR
KAPTTVSSLPDTKIEVAHFITKLLSYTKQLFRHGPF

233:

Human IL-5 (precursor)

MRMLHLHSL ALGAAVYVAI PTEIPTSALV KETLALLSTH RTLLIANETL RIPVPVHKNH
QLCTEEIFQG IGTLESQTVO GGTVERLFKN LSLIKKYIDG QKKKCGEERR RVNQFLDYLQEFGLVMNTEW
IIES

234:

Human IL-5 (processed)

I PTEIPTSALV KETLALLSTH RTLLIANETL RIPVPVHKNH
QLCTEEIFQG IGTLESQTVO GGTVERLFKN LSLIKKYIDG QKKKCGEERR RVNQFLDYLQ
EFLGMNTEW IIES

235:

Mouse IL-5 (processed)

MEIPMSTVVKETLQLSAHRALLTSNETMRLVPVTHKNHQLCIGEIFQGLDILKNQTVRGGTVEMLFQNLSLIKK
YIDRQKEKCGEERRRTRQFLDYLQEFGLVMSTEWAMEG

236:

CCL21 Swissprot: SY21_human: Sequence after cleavage of signal peptide:
SDGGAQD CCLKYSQRKI PAKVVRYSRK QEPSLGCSIP AILFLPRKRS QAELCADPKE LWVQQLMQHL
DKTPSPQKPA QGCRKDRGAS KTGKKGKGSK GCKRTERSQT PKGP

237:

CCL21 Swissprot: SY21_mouse: Sequence after cleavage of signal peptide:

105099.011002

SDGGGQD CCLKYSOKKI PYSIVRGYRK QEPSLGCPIP AILFSPRKHS KPCLCANPEE GWVQNLMRRL
DQPPAPGKQS PGCRRNRGTS KSGKKGKGSK GCKRTEQTQP SRG

238:

Swissprot: SDF1_human: Sequence after cleavage of signal peptide:

DGKPVSLSYRC PCRFFESHVA RANVKHLKIL NTPNCALQIV ARLKNNNRQV CIDPKLKWIQ
EYLEKALNKR PKM

239:

Swissprot: SDF1_mouse: Sequence after cleavage of signal peptide:

DGKPVSLSYRC PCRFFESHIA RANVKHLKIL NTPNCALQIV ARLKNNNRQV CIDPKLKWIQ
EYLEKALNKR

240:

BLC Sequences: Human: Accession: NP_006410

Amino acids 1-22 are signal peptide.

MKFISTSLLL MLLVSSLSPV QGVLEVYYTS LRCRCVQESS VFIPRRPIDR IQILPRGNGC
PRKEIIVWKK NKSIVCDPQ AEWIQRMMEV LRKRSSSTLP VPVFKRKIP

241:

BLC Sequence Mouse: accession: NP_061354

Amino acids 1-21 are signal peptide

MRLSTATLLL LLASCLSPGH GILEAHYTNL KRCRSGVIST VVGLNIIDRI QVTPPGNGCP
KTEVVIWTKM KKVICVNPR KWLQRLLRHV QSKSLSTPQ APVSKRRAA

242:

Human Eotaxin-1

1-23 is Signal peptide

1 mkvsaallwl llaaafspq glagpasvpt tccfnlanrk iplqrlesyr ritsgkcpqk
61 avifktklak dicadpkkkw vqdsmyldq kaptpkp

243:

Human Eotaxin-2

1-26 is Signal peptide

1 maglmtivts llflgvcahh iiptgsvvip spccmffvsk ripenrvvsv qlssrstclg

20050303 01:43:02

61 agvifttkkg qqfcgdpkqe wvqymknld akqkkaspra ravavkgpvq rypgnqtcc

244:

Human Eotaxin-3

1-23 is signal peptide

1 mmglslasav llasllslhl gtatrgsdis ktccfqyshk plpwtwvrsy eftsnsqsqr
61 avifttkrgk kvcthrpkkw vqkyisllkt pkql

245:

Mouse Eotaxin-1

1-23 is signal peptide

1 mqsstallfl lltvtsftsq vlahpgsipt secfimtssk ipntllksyk ritnnrctlk
61 aivfktrlgk eicadpkkkw vqdatkhldq klgtppk

246:

Mouse Eotaxin-2

1-25 is signal peptide

1 magsativag llllvacacc ifpidsvtip sscctsfisk kipenrvvsv qlangsicpk
61 agvifitkkg hkictdpkll wvqrhiqkld akknqpskga kavrtkfavq rrrgnstev

247:

M-CSF Sequence: human: the construct would be an N-terminal fragment consisting of residue 33 -181 or 33 -185, corresponding to the soluble form of the receptor.
Accession: NP_000748

MTAPGAAGRC PPTTWLGSLL LLVCLLASRS ITEEVSEYCS HMIGSGHLQS LQRLIDSQME
TSCQITFEFV DQEQLKDPVC YLKAFFLLVQ DIMEDTMRFR DNTPNATV QLOELSLRLK
SCFTKDYEEH DKACVRTFYE TPLQLLEKVK NVFNETHNLL DKDWNIFSKN CNNSFAECSS
QDVVTPKDCN CLYFKAIPSS DPASVSPHQP LAPSMAPVAG LTWEDSEGTE GSSLLPGEQF
LHTVDPGSAK QRPRSTCQS FEPPETPVVK DSTIGGSPQP RPSVGAFFNP MEDILDSAMG
TNWVPEASG EASEIPVQGW TELSPSRPGG GSMQTEPARP SNFLSASSPL PASAKGQQPA
DVTGTALPRV GFVRPTQGDW NHTPQKTDHP SALLRDPPEP GSPRISSPRE QGLSNPSTLS
AQPQLSRSHS SSVLPLGLH EGRSTRDRR SPAEPEGGPA SEGAAARLPR FNSVPLTDTH
ERQSEGSSEP QLESVFHLL VPSVILVLLA VGGLLFYRWR RRSQEPQRA DSPLEQPEGS
PLTQDDRQVE LPV

248:

M-CSF Mouse sequence: Mature sequence starts at amino acid 33. Accession.
NP_031804

MTARGAAGRC PSSTWLGSRL LLVCLLSRS IAEVSEHCS HMIGNHLKV LQOLIDSQME
TSCQIAFEFV DQEQLDPPVC YLKAFFLLVQ DIIDETMRFK DNTPNANATE RLQELSNLNL
SCFTKDYEEH NKACVRTFHE TPLQLLEKIK NFNETHNLL EKDNITPTKN CNNSFAECSS
RDVVTKDCN CLYFKATPSS DPASASPHQP PAPSMAPLAG LAWDDSQRTG GSSLLPSELQ
LRIEDPGSAK QRPRSTCQT LESTEQPNHG DRLTEDSQPH PSAGGFVPGV EDILESSLGT

10050893-011002

NWVLEEASGE ASEGFLTQEA KFSPTFVGG SIQAETDRPR ALSASFPFKS TEDQKPVDIT
DRPLTEVNPM RPIGQTONNT PEKTDGTSTL REDHQEPGSP HIATPNPQRV SNSATPVAQL
LLPKSHSWG I VLPLELEGK RSTRDRRSPA ELEGGSASEG AARPVARFNS IPLTDTGHVE
QHEGSSDPQI PRESVPHLLVP GIILVLLTVG GLLPYKWKWR SHRDPTLDS SVGRPEDSSL
TQDEDRQVEL PV

249:

Sequence of Human Resistin: Precursor.

MKALCLLLL PVLGLLVSSKTLCSMEEAINERIQEVAGSLIFRAISSIGLEQCQSVTSRGDLATCPRGFAVTGCTCG
SACGSDVRAETTCHCQCAGMDWTGARCCRVQP

250:

Sequence of Mouse Resistin: Precursor.

MKNLSFPLLFLFVPELGGSMPLCPIDEAIDKKIKQDFNSLFPNAIKNIGLNCWTVSSRGKLASCPEGTAVLSCSC
GSACGSDIREEKVCHCQCARIDWTAARCKLQVAS

251:

Lymphotoxin-β:

Swissprot: TNFC_human: Sequence of the extracellular domain:

QD QGGLVTETAD PGAQAQQLG FQKLPEEEPE TDLSPGLPAA HLIAGPLKGQ GLGWETTKEQ
AFLTSTQFS DAEGALPQD GLYLYCLVG YRGRAPPGGG DPQGRSVTLR SSLYRAGGAY GPGTPELLE
GAETVTPVLD PARRQGYGL WYTSVGFGL VQLRRGERV VN

252:

Lymphotoxin-β:

Swissprot: TNFC_mouse: Sequence of the extracellular domain:

QD QGRRVEKIIG SGAQAQKRLD DSKPSCILPS PSSLSETPDP RLHPQRSNAS RNLASTSQGP
VAQSSREASA WMTILSPAAD STPDPGVQQL PKGEPTDNL PELPAHLIG AWMSGQGLSW
EASQEEAFLR SGAQFSPTHG LALPDGVYY LYCHVGYRGR TPPAGRSRAR SLTLRSALYR
AGGAYGRGSP ELLLEGAETV TPVVDPIGY SLWYTSVGFGL GLAQLRSGER VYVNISHPDM
VDYRGRKTFE GAVMVG

253:

RNA-phage PP7:

msktivlsvg eatrtlteiq stadrqifee kvglplvgrlr ltslrqnga ktayrvnlkl
dgadvdcst svcgelpkvr ytgwshdvt ivansteasr ksyldtlksl vatsqveldv
vnlvplgr

254:

RNA-phage SP A1 protein:

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aklnqvtls kigkngdqtll tltprgvnpt ngvaslseag avpalekrvt vsvaqpsrnr
knfkvqiklq nptactrdac dpsvtrsafa dvtslftsyz tdeeralirt elaaladpl
ivdaidnlpl aywaallvas sgggdnpdp dvppvdpvkp pdgtgrykcp facyrlgsiy
evgkegsdpdi yergdevsvt fdyaedflg ntnwrnwdqr lsdydianrr rcrngnyidl
datamqsddf vlsgrgyvrk vkfpgafgsi kyllniqgda wldlsevtay rsygmvigfw
tdskspqlpt dftqfnsanc pvqtviips l

255:

"Qβ 240":

AKLETVTLGNIGRDGKQTLVLNPRGVNPTNGVASLSQAGAVP
ALEKRVTVSVSQPSRNRKKNYKVQVKIQNPTACTANGSCDPSVTRQ
KYADVTFSTQYSTDEERAFVRTELAALLASPLLDIDAIDLNPAY

256:

"Qβ 243":

AKLETVTLGKIGKDGKQTLVLNPRGVNPTNGVASLSQAGAVP
ALEKRVTVSVSQPSRNRKKNYKVQVKIQNPTACTANGSCDPSVTRQ
KYADVTFSTQYSTDEERAFVRTELAALLASPLLDIDAIDLNPAY

257:

"Qβ 250":

ARLETVTLGNIGRDGKQTLVLNPRGVNPTNGVASLSQAGAVP
ALEKRVTVSVSQPSRNRKKNYKVQVKIQNPTACTANGSCDPSVTRQ
KYADVTFSTQYSTDEERAFVRTELAALLASPLLDIDAIDLNPAY

258:

"Qβ 259":

ARLETVTLGNIGKDGKQTLVLNPRGVNPTNGVASLSQAGAVP
ALEKRVTVSVSQPSRNRKKNYKVQVKIQNPTACTANGSCDPSVTRQ
KYADVTFSTQYSTDEERAFVRTELAALLASPLLDIDAIDLNPAY

259:

"Qβ 251":

AKLETVTLGNIGKDGKQTLVLNPRGVNPTNGVASLSQAGAVP
ALEKRVTVSVSQPSRNRKKNYKVQVKIQNPTACTANGSCDPSVTRQ
KYADVTFSTQYSTDEERAFVRTELAALLASPLLDIDAIDLNPAY

260:

PH19 (SEQ ID NO:260)

1000000.01500

TAAGTCCTCTGCCACGTACC

261:

PH20 (SEQ ID NO:261)

TGGAAACCACGCTCACTTC

262:

PH21 (SEQ ID NO:262)

CGGGATCCGGGATGAAGAACCTTTCATTTC

263:

PH22 (SEQ ID NO:263)

GCCTCTAGAGAGGAAGCGACCTGCAGCTTAC

264:

PH29 (SEQ ID NO:264)

CTAGCGGGAGGGGGTGGATGTGGGGACGACTACAAGGATGACGACA

265:

PH30 (SEQ ID NO:265)

AGCTTGTCTCATCCTTGTAGTCGTCCCCACATCCACCCCTCCCG

266:

PH31 (SEQ ID NO:266)

AGCTTACTCACACATGCCACCGTGCCAGCACCTGAAGCCGAGG

267:

PH32 (SEQ ID NO:267)

CGGCTTCAGGTGCTGGGCACGGTGGGCATGTGTGAGTA

268:

1050393.011302

PH35 (SEQ ID NO:268)

CTAGCGGGAGGGGGTGGATGTGGGATCGAAGGTCGCA

269:

PH36 (SEQ ID NO:269)

AGCTTGCACCTTCGATCCCACATCCACCCCTCCCG

270:

PH37 (SEQ ID NO:270)

CGGGATCCAGCAGCTGGGCTCGAGGTGCTAGCTTTGTTAAAC

271:

PH38 (SEQ ID NO:271)

GATCGTTTAAACAAACAAAGCTAGCACCTCGAGCCCAGCTGCTGGATCCCGGTAC

272:

PH39 (SEQ ID NO:272)

CTAGCGGGAGGGGGTGGATGTGGGGACGATGACGACA

273:

PH40 (SEQ ID NO:273)

AGCTTGTGTCATCGTCCCCACATCCACCCCTCCCG

274:

PH41 (SEQ ID NO:274)

CATGGAGACAGACACACTCCTGCTATGGGT

275:

PH42 (SEQ ID NO:275)

1050000.017500

GCAGTACCCATAGCAGGAGTGTGTCTGTCTCCATGGTAC

276:

PH43 (SEQ ID NO:276)

ACTGCTGCTCTGGGTTCCAGGTTCCACTGGTGACGCG

277:

PH44 (SEQ ID NO:277)

GATCCGCGTCACCAGTGGAACCTGGAACCCAGAGCA

278:

SU7 (SEQ ID NO:278)

AGCTTGCGGATCCAGGATATCGGCTCGAGGTTCTAGAGTG

279:

SU8 (SEQ ID NO:279)

GGCCCACTCTAGAACCTCGAGCCGATATCCTGGATCCGCA

280:

Resistin-C-Xa:

SSMPLCPIDEAIDKKIKQDFNSLFPNAIKNIGLNCWTVSSRGKLASCPEGTAVLSCSCG
SACGSWDIREEKVCHCQCARIDWTAARCKLQVASSLAGGGGCGIEGR

281:

Resistin-C-EK

SSMPLCPIDEAIDKKIKQDFNSLFPNAIKNIGLNCWTVSSRGKLASCPEGTAVLSCSCG
SACGSWDIREEKVCHCQCARIDWTAARCKLQVASSLAGGGGCGDDDD

282:

Resistin-GCG:

SSMPLCPIDEAIDKKIKQDFNSLFPNAIKNIGLNCWTVSSRGKLASCPEGTAVLSCSCG
SACGSWDIREEKVCHCQCARIDWTAARCKLQVASSLAGGGGCG

1050800.011002

283:

pCep-Xa-F*: (complete sequence)

1 GCGCCGCGCG CGGACGAACT AAACCTGACT TGCCCTCTTCT TCGCTGTGTAC GAGGAGCGCT
71 TTGTTTGTGTT ATCTGGGGGA GTGCAATGTAA TCCCTTTCAGT TGCTTGGTAC AACTTGCCAA CTGGGCGCTG
141 TTCCACATGT GACATGGGGG GGGGACCAAC TTTCATCTCT GACGAGACTT TGCATCTGT GGACTCGAAC
211 GGATGTCGAC ATTGCCAC ACTGATGAGT GAGGAGCTCT AACCAATGCT TGGGGGACAT GTAACCTCCA
281 ACAACATGCG CTTTATGTGT AACTCTTGGC TGGAGCTCTT ACACCAATGT TGGGGGACAT GTAACCTCCA
351 GGGGGCCAGG AAGACTACGG GAGGCTACAC CAACTGTCAAT CAGAGGGGCC CTGTATAGTA CGGATAGGG
421 GCGGCTCAAG AGGGCATTAG CAATAGTGT TTATAGGGCC CTCTGTTTAA CTAAGAGGTT CAGTATAGCG
491 TTCCGGGGTA ATGATATATA CTATCCAGAC TAAACCTAAT TCAATAGCAT ATGTATACCA ACGGGAGBGA
561 TATGCTATCG ATATAGGGTT AGTAAAGGG TCTTAAGGGA CAGGATATCT TCCACGCCA TGGAGTGTCA
631 CGGTTTATT TACATGGGT CAGATGCCA CCGGGTAGT GAACTATT TTACTACAAG CGAGTGGCTG
701 AAGATCAAGG AGCGGGCAGT GAACTCTCTT GAATCTCTCG CTGCTTCTTC ATTCTCTCTT GTTTAGCTAA
771 TAGAATAAGT GCTGAGTGT GAACAGTAG GTGTATGTGA GTGTCTGAA GTGTCTGAA CACCAATATA ACCCTCACAA
841 CCCCAGAATA AAATTTGGAC GGGGGGTTCA GTGGTGGCAT TGTGCTATGA CACCAATATA ACCCTCACAA
911 ACCCTCTGGG CAATAAATAC TAGTGTAGGA ATGAACAATT CTGAATATCT TTAACAATAG AAATCCATGG
981 GGTGGGGACA AGCGGTAAAG ACTGAGTGTCT CATCTCACAC GAATTTATGG ATATTTATGG CACATATCC
1051 TACTGCATA TGAATCTGG GTTATTAAGA TGTCTCCAG CAGGAGACCA ACACCAATCT GTTCTCTCTT
1121 TACATCTTAT TTGTAAACAG GGGAAAGAGA GTGGAGCGCG ACAGCAGCGG ACTCCACTG TGTCTCTAA
1191 CACCCCGGAA AATTAACCGG GGCTCCACCG CAATGGGGCG CATPAACAAA CAGAAGTGGC CACTCTTTTT
1261 TTGTAAATTG TGGAGTGGGG GCACGGCTCA GCGCCACAC GCGCCCTGCT GTTTTGACG TGTAAATAAA
1331 GGGTGAATA ACTTGGCTGA TTGTAAACCC GCTAACCACT GGGGTCAAC CACTTGGCCA CAAAACCACT
1401 ATGTGCAATG CGGGAAATAC CTGCTAAGT AGGTGGGGG CGGCAGATAG GGGCGCAATT CTGCTCAATCT
1471 GGGAGACAA TTACACAGC TTGGCTCTGA GCGCCACCA CAGGTGTCTT GGTCTCTCTT TCCAGAGGT
1541 CGCTGAGAGC AGGTGGGCT AATGTTGCCA TGGGTAGCAT ATACTACCCA AATATCTGGA TAGCATATGC
1611 TATCTTAATC TATGCTGGG TAGCATAGGC TATCTTAATC TATCTTGGG TAGCATATGC TATCTTAATC
1681 TATATCTGGG TAGTATATGC TATCTTAATC TATATCTGGG TAGCATATGC TATCTTAATC TATATCTGGG
1751 TAGCATATGC TATCTTAATC TATATATGC TATATATGC TATCTTAATC TATCTTAATC TATCTTAATC
1821 TATCTTAATC GAGATATGGG TAGTATATGC TATCTTAATC TATCTTAATC TATCTTAATC TATCTTAATC
1891 CTGTGACAA ATATCTGAG TATCTTAATC TATCTTAATC TATCTTAATC TATCTTAATC TATCTTAATC
1961 ATAGGTATCT CTAACTCTATA TCTTGGTAGC ATATGCTATC CTAACTCTATA TCTTGGTAGC ATATGCTATC
2031 CTAACTCTATA TCTTGGTAGC ATAGGTATCT CTAACTCTATA TCTTGGTAGC ATATGCTATC CTAACTCTATA
2101 CTAACTCTATA TCTTGGTAGC ATAGGTATCT CTAACTCTATA TCTTGGTAGC ATATGCTATC CTAACTCTATA
2171 ATATGATACG CAGTATAGA GTGGGAGTGC TATCTTTGCT ATATGCTGCG ACCTTCCAA GGGGGGTGAA
2241 TTTTCTGCTG TGTCTTTTTT CTGCTATGCT GGTGCTGCTG ATCTTATGCT GAACTTAAGG AGGCGCAGCT
2311 AAAGCGCTGC CATCTCTGAT TGTCTCACG GTAAATGTGG CTAAATTTTT CAAACCGAG AAGGTGTGGA
2381 GCGCGAGACT GAGTGAAGTG ACAACATGGG TATGCGCAAT TGCCCAATGT TGGGAGGACG AAAATGTGTA
2451 CAGAGAGACT GCGCAGAAAT ACACCAACAG CAAGCATGAT GTCTACTGGG GATTTATTT TTAGTGCGGG
2521 GGAATACAGC GCTTTTAAAT CGATTAGGG CGTCTCCTAA CAGTATCAT ACTCTCTGCG CTCTCTCAAC
2591 CTCACTTCCA TCACTCTCTT CATCTCTGCT ATCTCTGCTA TCACTCTGCT TCACTCTGCT TCACTCTGCT
2661 GTGGGAALCC AGGAGGGCAA ATCTACTCCA TGGTCAAAG TGACACAGAT TCACTCTGCT TCACTCTGCT
2731 GAGCGGCTCT TGTATATACA AGGTGCTTAA TGGCATCTT CAATACCTCA CAAATATAT GAGTTGTGTA
2801 AAGACCATG AATAACAGA CAATGAGACT CCTTAGCGGG CCGGCGGTCT AGGGCGCATT
2871 CAAAGGGGGA GACGACTCAA TGGTGTAAAG CGACATTTGT GAATAGCAAG GCGACTCTCT CGCTTAGGT
2941 TGTAAAGGGA GTCTTACTTA CTTCCATATA CGAACACAC GGGGACCCA GTTCTCTGCT GTTCTCTGCT
3011 TTCTAGGTGA CTCTTAGCCA GGAGAGCTCT TAAACCTCT GCAATTTCTT CAAATTTCTG GTTGAAGGTA
3081 CTGTGACAA ATCTCTTCTT JAACACACT CTCTTTTGTG CTCTTCTGCT AGCTGCTCTC CCGCGGCTCT
3151 CAGTGTCTCT GGTCTCTCTT GGTCTCTCTT GGTCTCTCTT GGTCTCTCTT GGTCTCTCTT GGTCTCTCTT
3221 ACATCTGCGG CCACTCTCTT GGTGTATCTT AAAATATCTG GTTCTCTCTT CAGGGGTGAA AAGGCGCTCT
3291 CTACTGCGGG GGGGCTGCGG CGGTGGAGAC CGGTGATGAT ATGACTGACT ACTGGGACTA CTATGGCTCT
3361 TTCTCTCAGC TCCACGACTC CTCCCTCTGG CTCTTTCAG ACTTCTCTCTT CTGCTCTCTT CAGCTCTCTT
3431 ACCCGGCGCG CTCTCACTAC CTCTCTGAGC CGGCTCTCTA CTACTCTCTT CTACTCTCTT CTACTCTCTT
3501 CTCTGAGCCT CTCTCTGAG CTCTCTGAGC CTCTCTGAGC CTCTCTGAGC CTCTCTGAGC CTCTCTGAGC
3571 CTGCGCTCTG TCTCTCTGCG CTCTCTGCGC CTCTCTGCGC CTCTCTGCGC CTCTCTGCGC CTCTCTGCGC
3641 TCTCTGCGCT CTCTCTGCGC CTCTCTGCGC CTCTCTGCGC CTCTCTGCGC CTCTCTGCGC CTCTCTGCGC
3711 CTCTGCGCTCT CTCTCTGCGC CTCTCTGCGC CTCTCTGCGC CTCTCTGCGC CTCTCTGCGC CTCTCTGCGC
3781 CTCTGCGCTCT CTCTCTGCGC CTCTCTGCGC CTCTCTGCGC CTCTCTGCGC CTCTCTGCGC CTCTCTGCGC
3851 TCTCTCTGCG CTCTCTGCGC CTCTCTGCGC CTCTCTGCGC CTCTCTGCGC CTCTCTGCGC CTCTCTGCGC
3921 CTCTCTGCGC CTCTCTGCGC CTCTCTGCGC CTCTCTGCGC CTCTCTGCGC CTCTCTGCGC CTCTCTGCGC
3991 CCGCTCTGCG CTCTCTGCGC CTCTCTGCGC CTCTCTGCGC CTCTCTGCGC CTCTCTGCGC CTCTCTGCGC
4061 TCTCTCTGCT GCGCTCTGCT CCGCTCTGCT CCGCTCTGCT CCGCTCTGCT CCGCTCTGCT CCGCTCTGCT
4131 CCGCTCTGCT GCGCTCTGCT CCGCTCTGCT CCGCTCTGCT CCGCTCTGCT CCGCTCTGCT CCGCTCTGCT
4201 CTGCTCTGCT GCGCTCTGCT CCGCTCTGCT CCGCTCTGCT CCGCTCTGCT CCGCTCTGCT CCGCTCTGCT
4271 TTTTGGGGT CTCTGAGAC CATCTCTATG CTCTGAGCCT CTCTGAGCCT CTCTGAGCCT CTCTGAGCCT
4341 CCGCTCTGCT GCGCTCTGCT CCGCTCTGCT CCGCTCTGCT CCGCTCTGCT CCGCTCTGCT CCGCTCTGCT
4411 TGGCGCGGCA GCGCTCTGCT CCGAGATGCT CTCTCTCTCT TCTTAGGCCA TTTTCAAGGT CTGTACGTG
4481 CCGCTCTGCT GCGCTCTGCT CCGAGATGCT CCGAGATGCT CCGAGATGCT CCGAGATGCT CCGAGATGCT
4551 CAGGAGAGTGC AGACTCTGCG CCGCTCTGCG CCGCTCTGCG CCGCTCTGCG CCGCTCTGCG CCGCTCTGCG
4621 AGATGCAAGT CTGAAATATC CCGACTCTG CCGACTCTG CCGACTCTG CCGACTCTG CCGACTCTG
4691 AAATCTCTG CTGAAATATC CCGACTCTG CCGACTCTG CCGACTCTG CCGACTCTG CCGACTCTG
4761 CTCTCTGCTG GAGCTTAGGG ATGAGATATC TCGGGAGATC TCGGGAGATC TCGGGAGATC TCGGGAGATC
4831 GATGCTCTG GGGCAACGGA AGAAAGACTG GGTGCGGCT GTGAGGATAT GTTATCTGAT GATGAGCTGT

4901 CAAACATGAG AATTCTTGAA GACGAAAGGG CCTCGTGATA CGCCTATTTT TATAGGTTAA TGTCATGATA
 4971 ATATAGTGTTT CTTAGACGTC AGGTGGCACT TTTCGGGGAA AACCCCTATT TGTGTTTATT
 5041 TCTAATAACA TGATATATTC TATTCGCGTCA TGAGACAATA ACCCTGATGA TCTCTTCAAT AATATGTAAA
 5111 AAGGAGAGAT ATGATATATC AACATTTTGG CTTCGGCCCT ATTCCCTTTT TTGGCGATT TTGGTATGCT
 5181 GTTTTATGTC ACACGAAAC GTCTGTGAAA TAAAGAGATG CTGAAGTACA GTTGGGTGCA CGAGTGGGTT
 5251 ACATCGAAGT GGATCTCAAC ACCGCTAAGA TCCTTGAGAG TTTCGGCCCC GAAGAAAGTT TTCCAATGAT
 5321 GAGCACTTTT AAGTCTCTGC TATGTGGCGC GTTATTATCC CGTGTGGACG CGGGCGAAGA GCACATCGGT
 5391 CGCCGATAC ATCAATTTCA GAATGACTTG GTTGAAGTACT ACCAGATCAC TTCAACGATG
 5461 GCATGACAGT AAGAGAAATA TGCAAGTCTG CCAATACCAT GAGTGAATAC ACTCGCGCCA ACTTACTTCT
 5531 GACAGAGGTC GGAGAGACGA AGAGACTTAAC CTTCTTCAAT GACAGATGAG CTTCTTCAAT AGCTGATGCT
 5601 GATCTGATCT ACACGAGATC GAATGAAGCC ATACCAALAG ACAGCGGTGA CACCAAGATG CTCGACGAAA
 5671 TGCGACCAAC GTTGGCCAAA CTATTAAGTC GCGAATCACT TACTCTAGCT TCCGGCGAAC AATTAATAGA
 5741 CTGATAGTAG GCGGTAAAG TTGCAGGACC ACTCTGCGCT TGCGCCCTTC CGCGGCTGCT GTTTATTGCT
 5811 GATAAATCTG GAGCGGGTGA GCGTGGGTCT CGCGGTATCA TTGCAGCATC GGGGCGAGAT GATAGGCCCT
 5881 CGCGATACGT AGTTATCTAC ACAGCGGGGA GTTCAGGCAAC TATGAGTGA TGAATATAG AGATCGCTGA
 5951 GATAGGTGCC TCACATGATA AGCATTTGTA ACTGTGAGC AAGTTTACT CATATATACT TTAGATTTGAT
 6021 TTAAGACCTC ATTTTATATT TAAAGATC TAGGTGAAGA TCTCTTTTGA TACTCTGAG ACCAAATCTG
 6091 CTAAACGTGA GTTTTCTGTC CACTGAGCTC GACACCCTGT AGAAAGATC AAGATGATT CTTGAGATCC
 6161 TTTTTTCTG CGGTAAATCT GCTGCTTGCA AACAAAAAAA CACCGCTAC CAGCGGTGCT TATTTTGCGG
 6231 GATCAAGAGC TACCAACTCT TTTTCCGAAG GTAACTGTCT TCAGCAGAGC GCAGATAGTA AGTGTGCTG
 6301 TCTAGTGTA GCGTATGTA GGGCACTGCT TCAAGAACTC GTTAGCACC GCTACATACC TCCTCTGTCT
 6371 AATCTGTGTA CCAAGTGGCTG CTCACCAAGG CTGAAATGCTG TGCTTTACCG GTTTGGACTC AAGACATAG
 6441 TTACCGATGA GCGGACACG ACAGGATAC CTACAGCGTG AGCTATGAGA AAGCGCCACG TCTCCGAGG GGAAGAAAGC
 6511 CCTACACGTA ACAGGATGTC ACAGCGGGTT CTGACACGAC CTGTCACACA GCTTCACAGA GAGGACATGA
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 6651 TGGTATCTTT ATGATCCTGT CGGGTTTCGC CACCTCTGAC TTGAGCGTCC ATTTTTTGTA TGCTCTGAC
 6721 GCGGGCGGAG CTAATGAAAA AACGCGACGA CCGCGGCTTT TTAGCGTCTG TGCGGCTTTT GCTGGCGCGC
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 6861 CTGCGCAAGA TTGATGGGCT CAAATGTGTA GAGTGTGTTA TCGCTATGTA CAGATATCCA GCTCCGATCA
 6931 GAACATGCTG TATGATGTTT TATGATGTTT GGTGAAGTGT GTGGAAGTCT GCGTAAGCTC CACAGCAGCA
 7001 GAAGTATGCA AAGCATGTCAT CTCAATTAGT CAGCAACACG GTTGGGAAGT TCCCAGAGCT CCGCAGCAGG
 7071 CAGAAGTATG CAAGCATGCG ATCTCAATTA TCAGCAACCG ATATGTCGCG CCTCAATCC CCGCATGCTG
 7141 CCCTTAACCT CGGCCAGTTC GCGCAATCTC CGGCCCAATC GTGACTAAT TTTTTTTTAT TATGCAGAG
 7211 CCGAGGCGCG CTCGGCCCTT GAGCTATTCC AGAAGTAGTG AGAGGCTTTT TTGAGAGGCT GACGACCCAG
 7281 ACAGGCGGCG GCGGCGGCTG CAGTGTGCTC CAGTGAAGCA CTCACAGAGA CAGCACTCTC GCGTCCGCTG
 7351 TACAGAGCCA CCGTGCGCCT CGCCACCCCG GAGCAGTCC CCAGCGCCGT ACAGCAGCTC GCGCGCGCTG
 7421 TGCGGAGTCA CGGCGCCAC GCGCCACCG TCGACCCCGA CGGCGCATC GAGCGCGTCA CAGCGCTGCA
 7491 AGAAGCTCTC CTACGCGCGG TCGGGCTCGA CATCGGCAAG GTTGGGGTCC GGAACGACG CCGCGCGGTG
 7561 GCGGTCTGGA CACGCGCGGA GAGCGTGA GCGGCGGCGG TGTTTCGCGA GATCGGCCG CGCCTCGGCT
 7631 AGTTGAGCGG TTTCGCGCTG GCGCGCGAGC AACAGATGAG AGGCTCTCTG GCGCGCGACC GCGCCAGAGA
 7701 GCGCGTGGCT TTCTCGGCGA CGCTCGCGCT CTCGCGCGAC CACGAGGGCA AGGCTCTGGG CAGCGCGCTG
 7771 GTGCTCCGCG GAGTGGAGGC GCGCGAGGCG GCGCGGTGTC GCGCTCTTCT GAGAGACTCC GCGCCCGCGA
 7841 ACTCCGCCCT CTAGGAGCGG CTGCGCTTCA CGGTCAACCG GACGCTGAG TGCCCGAAG ACOCGCGGAC
 7911 CTGGTGCAAT GCGCGCAAGC CGGTCGCTG ACGCGCGCGC CAGCAGCCAG CAGCGCCAG GAAAGAGAGC
 7981 GCAAGAGGCTG CTCGCGAGCG GCGCCACGGG TCCGACGGGG GTGACCTCG GAACTTGTGT ATTGCAGCTT
 8051 ATATGAGTGA CAAATAAAGC AATAGCATCA CAATTTTAC AATTAAGTCA TTTTCTTAC TGCACTCTAG
 8121 TGTGTGGTGT TCGAACTCA TCAATGCTC TTATCTATC TATCATGCA AGCAGCCCTT CTCTGACAA
 8191 TCTCATGTT TGAACCTTTA TCATCSCAGA TCCGCGACAT GTTGTGCAT TGCTGAGCG GAGACAGCTG
 8261 TAGGTATGGA AGCTATATAC ATTGAATCAA TATTGGCAAT TAGCATATTG TATATAGCAT TATATGCTC
 8331 AATATCAAT TGGCTATTGG CCAATGCTCA CTGTGTATCT ATATCATAT ATGTACATTT ATTATGCTCT
 8401 ATATCCAAAT GAGCGCCAT GTTGAACATT ATTAATGACT ATTAATTAAT TAGCGGGTCA TAGCGGGTCA
 8471 TTAGTATCTA GCGCATATAT GGGTTCGCG GTTACATAT TACGGTAAA TCGGCTGCT GCGTCAAGCT
 8541 CCAACAGGAT CCGCGCATGT AGCTCATATA TCGGATGTTA TCCGATATTA ACCCATATAG GAGTCTTCCA
 8611 TTGAGTCTAA TGGTGGAGAT ATTACGTA AACTGCGGAC TTGGAGTAT ATCAAGTGA TCAATTTCCA
 8681 AGTCCGCCGC CTATTGAGCT CAATGACGGT AAATGGCCCG CCGTGCAATTA TGCCAGATAT ATGACTTAC
 8751 GGGACTTTTC TATTTGGCAG TACATCTACG TATTAGTCACT CGCTATTACC ATGTGATGC GTTTTGGCA
 8821 GTACACCAAT GGGCTGGAT AGCGGTTTGA CTCACGGGGA TTTCGAACTG TCCACCCCAT TGAGCTCAAT
 8891 GGGAGTTTGT TTGGCACCAC AAATCACAG GACTCTGAGT AATGCTGAAA TATGCTGAGT TATCCCGC
 8961 AATAGCGCG TAGCGTGTGA TCGGCGAGG TCTATATAG CAGAGCTCG TTAGTGAAAC CTGACATCTC
 9031 TTAGAGCTGG GTACCGGGAT CCGAGCAGCT GGCTCGAGGT GCTAGCGGGA GGGGTTGAT GTGGAGTGA
 9101 AGGTGCGAAG CTTACTACCA CATGCCAAC GTGCCACCG CTGGAAGCG AGGGGCGAC CTGACCTCTC
 9171 CTCTCCCGCC CAUAAACCCA GGCACCCCTC ATGATCTCCC GGACCCCTGA GTGCATGCT GTAGTGTGTG
 9241 AAGTAGGCGA GAGAACACCT GAGGTCAAGT TCAACTGCTA GTTCGAGCGC GTTCGAGGTG ATATAGCGAA
 9311 GACAAAGCGG GGGAGGAGCG GAGTCAAGAG CACTCTGAGT TCGGTGAGCG GTGTGAGCG CTCTGACCTC
 9381 GACTGGCTGA AGTGCAGAGA GTACAGTGTG AAGTGTCCA ACAAGCCCTT CCGACGCTCT CACGAGAAA
 9451 CCATCTTCCA AGCCAAAGGG CAGCGCCGAG AACCAAGGT GTACACCCCT GCGCCATCCC GGGATGAGCT
 9521 GACCAACACG CAGGTGACCC TGAOCTGCTT GGTCAAAGGC TTCTATCCA CGGACATGCG CGTGGAGTGG
 9591 GAGAGCAATG GAGCGCGGGA GAACACTAC AAGACCACG CTCGCTGTG GAGCTCCGAG CTTCTCTCT
 9661 TCTCTTACAG CAGCTGACCC GTGCGAAGA CAGGTTGSCA GCGAGGGAAC GTCTCTCTAT CTTCTCGTAT
 9731 GCTTAGAGGCT TTGGGACGAG AACTACAGC ACTACAGCA AGAGAGATCT GAATAGCGCT GTGCACATC ATCATATCA
 9801 CCAACAGCTA CTGATCTGAG TGAAGATCTT GAATAGCGCT GTGCACATC ATCATATCA TTTAGTGGT
 9871 TNAACGATTC AGACATGATA AGATACATTG ATGAGTTTGG ACAAAACACA ACTAGAATAG AATGAAAAAT
 9941 ATGCTTATT TTGGAATTT TTGATGCTAT TGCTTTATT GTAAACATTA TGAATGCAA TAAGTAAAG
 10011 AACACAAACA ATTGCTATCA TTTTATGTT CAGGTCGAGT GGGAGGTGGG GAGGTTTATT AAGAGTAAA
 10081 AACCTCTAC AATATGTGTA TGCTGATATA TGATCCGCGT CTTGCGGCG GTTGGGTGAT GAGGTGAAA
 10151 ACTTACCTC CCGAAGACCT CCGAAGACCT TCAACAGTGC TCTGTAGCG GATGCGGGG GCGAGGAGC
 10221 CGTCAAGGC GGTGAGCGG GTGTGGCGG GTTCTGGGCG GACGACATGA CCGGTGACT CTAGA

284:

5'LT• : (SEQ ID NO:284)

5'-CTT GGT GCC GCA GGA TCA G-3'

285:

3'LT• : (SEQ ID NO:285)

5'-CAG ATG GCT GTC ACC CCA C-3'

286:

5'LT• long-*NheI*: (SEQ ID NO:286)

5'-GCC CGC TAG CCT GCG GTG GTC AGG ATC AGG GAC GTC G-3'

287:

5'LT• short-*NheI*: (SEQ ID NO:287)

5'-GCC CGC TAG CCT GCG GTG GTT CTC CAG CTG CGG ATT C -3'

288:

3'LT• stop-*NotI*: (SEQ ID NO:288)

5'-CAA TGA CTG CGG CCG CTT ACC CCA CCA TCA CCG -3'

289:

GST-EK-C-LT•₄₉₋₃₀₆: SEQ ID NO:289

APLVMSPILGYWKIKGLVQPTRLLLEYLEEKYEEHLYERDEGDKWRNKKFELGLEFPNLPYYIDGDVKLTQ
SMAIIRYIADKHNMMLGGCPKERAIEISMLEGAVLDIRYGVSR IAYSKDFETLKVDFLSKLP EMLKMFEDRLCH
KTYLNGDHDVTHPDFMLYDALDVLVYMDPMCLDAFPKLVCFKKRIEAI PQIDKYLKSSKYIAWPLQGWQATF
GGGDHPPKASMTGGQQMGRDLYDDDDKLACGGQDQGRRVEKIIGSGAQAKRLDDSKPSCILPSPSSL
SETPDPRLHPQRSNASRNLASTSQGPVAQSSREASAWMTILSPAADSTPDPGVQQLPKGEPETDLNPEL
PAAHLIGAWMSGQGLSWEASQEEAFLRSGAQFSPTHGLAL PQDG VVYLYCHVG YRGRTPPAGRSRARS
LTLRSALYRAGGAYGRGSP ELLLEGAETVTPVVDPIGYGSLWYTSVGFGLAQLRSGERVVYNISHPDMV
DYRRGKTFFGAVMVG

290:

GST-EK-C-LT•₁₂₆₋₃₀₆: SEQ ID NO:290

APLVMSPILGYWKIKGLVQPTRLLLEYLEEKYEEHLYERDEGDKWRNKKFELGLEFPNLPYYIDGDVKLTQ
SMAIRYIADKHNMLGGCPKERAISMLEGAVLDIRYGVSRAYSQDFETLKVDFLSKLPMLKMFEDRLCH
KTYLNGDHVTHPDFMLYDALDVVLYMDPMCDAFPKLVCFKKRIEAIQIDKYLKSSKIYAWPLQGWQATF
GGGDHPPKASMTGGQQMGRDLYDDDDKLACGGSPAADSTPDGPVQQLPKGEPETDLNPPLAAHLIGA
WMSGQGLSWEASQEEAFLRSGAQFSPTHGLALPQDGVYYLYCHVGYRGRTPPAGRSRARSRTLRSALY
RAGGAYGRGSPELLEGAETVTPVVDPIGYGSLWYTSVGFGLAQLRSGSERVYVNISHPDMVDYRRGKT
FFGAVMVG

291:

his-myc-EK-C-LT⁴⁹⁻³⁰⁶: SEQ ID NO:291

APLVHHHHHHGPLVDVASNEQKLISEEDLASMTGGQQMGRDLYDDDDKLACGGQDQGRRVEKIIGSGAQ
AQKRLDDSKPSCILPSPSSLSETPDPRLHPQRSNASRNLASTSQGPVAQSSREASAWMTILSPAADSTPDGPV
QQLPKGEPETDLNPPLAAHLIGAWMSGQGLSWEASQEEAFLRSGAQFSPTHGLALPQDGVYYLYCHVGY
RGRTPPAGRSRARSRTLRSALYRAGGAYGRGSPELLEGAETVTPVVDPIGYGSLWYTSVGFGLAQLRSG
ERVYVNISHPDMVDYRRGKTFFGAVMVG

292:

his-myc-EK-C-LT¹²⁶⁻³⁰⁶: SEQ ID NO:292

APLVHHHHHHGPLVDVASNEQKLISEEDLASMTGGQQMGRDLYDDDDKLACGGSPAADSTPDGPVQQLP
KGEPETDLNPPLAAHLIGAWMSGQGLSWEASQEEAFLRSGAQFSPTHGLALPQDGVYYLYCHVGYRGRTP
PPAGRSRARSRTLRSALYRAGGAYGRGSPELLEGAETVTPVVDPIGYGSLWYTSVGFGLAQLRSGSERVY
VNISHPDMVDYRRGKTFFGAVMVG

293:

primerMCS-1F

5'-TAT GGA TCC GGC TAG CGC TCG AGG GTT TAA ACG GCG GCC GCA T-3' (SEQ ID NO:293)

294:

primerMCS-1R

5'-TCG AAT GCG GCC GCC GTT TAA ACC CTC GAG CGC TAG CCG GAT CCA-3' (SEQ ID NO:294)

295:

Bamhis6-EK-Nhe-F

5'-GAT CCA CAC CAC CAC CAC CAC GGT TCT GGT GAC GAC GAT GAC AAA GCG CTA GCC C-3'
(SEQ ID NO:295)

1050398.01502

296:

Bamhis6-EK-Nhe-R

5'-TCG AGG GCT AGC GCT TTG TCA TCG TCG TCA CCA GAA CCG TGG TGG TGG TGG TGT G-3'
(SEQ ID NO:296)

297:

oligo1F-C-glycine-linker

5'-TCG AGG GTG GTG GTG GTG GTT GCG GTT AAT AAG TTT AAA CGC-3' (SEQ ID NO:297)

298:

oligo1R-C-glycine-linker

5'-GGC CGC GTT TAA ACT TAT TAA CCG CAA CCA CCA CCA CCC-3' (SEQ ID NO:298)

299:

oligo1F-C-gamma1-linker

5'-TCG AGG ATA AAA CCC ACA CCT CTC CGC CGT GTG GTT AAT AAG TTT AAA CGC-3' (SEQ ID NO:299)

300:

oligo1R-C-gamma1-linker

5'-GGC CGC GTT TAA ACT TAT TAA CCA CAC GGC GGA GAG GTG TGG GTT TTA TCC-3' (SEQ ID NO:300)

301:

oligo1FA-C-gamma3-linker

5'-TCG AGC CGA AAC CGT CTA CCC CGC CGG GTT CTT CTG-3' (SEQ ID NO:301)

302:

oligo1RA-C-gamma3-linker

5'-CAC CAC CAG AAG AAC CCG GCG GGG TAG ACG GTT TCG GC-3' (SEQ ID NO:302)

1050306-011602

303:

oligo2FB-C-gamma3-linker

5'-GTG GTG CTC CGG GTG GTT GCG GTT AAT AAG TTT AAA CGC-3' (SEQ ID NO:303)

304:

oligo2RB-C-gamma3-linker

5'-GGC CGC GTT TAA ACT TAT TAA CCG CAA CCA CCC GGA G-3' (SEQ ID NO:304)

305:

rMIF-F

5'-GGA ATT CCA TAT GCC TAT GTT CAT CGT GAA CAC-3' (SEQ ID NO:305)

306:

rMIF-Xho-R

5'-CCC GCT CGA GAG CGA AGG TGG AAC CGT TC-3' (SEQ ID NO:306)

307:

rMIF-C1:

MPMFIVNTNVPRASVPEGFLSELTQQLAQATGKPAQYIAVHVVPDQLMTFSGTSDPCALCSLHSIGKIGGAQ
NRNYSKLLCGLLSDRLHISPDVYINYYDMNAANVGWNGSTFALEGGGGCG (SEQ ID NO:307)

308:

rMIF-C2

MPMFIVNTNVPRASVPEGFLSELTQQLAQATGKPAQYIAVHVVPDQLMTFSGTSDPCALCSLHSIGKIGGAQ
NRNYSKLLCGLLSDRLHISPDVYINYYDMNAANVGWNGSTFALEDKTHTSPPCG (SEQ ID NO:308)

309:

rMIF-C3

MPMFIVNTNVPRASVPEGFLSELTQQLAQATGKPAQYIAVHVVPDQLMTFSGTSDPCALCSLHSIGKIGGAQ
NRNYSKLLCGLLSDRLHISPDVYINYYDMNAANVGWNGSTFALEPKPSTPPGSSGGAPGGCG (SEQ ID
NO:309)

10650698.011802

MPMFIVNTNVP RASVPDGFSL ELTQQLAQAT GKPPQYIAVH VVPDQLMAFG GSSEPCALCS
LHSIGKIGGA QNRSYSKLLC GLLAERLRIS PDRVYINYD MNAANVGWNN STFALEGGGGGCG

PMFIVNTNVP RASVPDGFLS ELTQQLAQAT GKPPQYIAVH VVPDQLMAFG GSSEPCALCS
LHSIGKIGGA QNRSYSKLLC GLLAERLRIS PDRVYINYVD MNAANVGWNN STFALEGGGGGCG

MPMFIVNTNVP RASVPDGLFLS ELTQQLAQAT GKPPQYIAVH VVPDQLMAFG GSSEPCALCS
LHSIGKIGGA QNRSYSKLLC GLLAERLRIS PDRVYINYD MNAANVGWNN STFALEDKTHTSPPCG

PMFIVNTNVP RASVPDGLFS ELTQQLAQAT GKPPQYIAVH VVPDQLMAFG GSSEPCALCS
LHSIGKIGGA QNRSYSKLLC GLLAERLRIS PDRVYINYYD MNAANVGWNN STFALEDKTHTSPPCG

MPMFIVNTNVP RASVPDGLFLS ELTQQLAQAT GKPPQYIAVH VVPDQLMAFG GSSEPCALCS
LHSIGKIGGA QNRSYKLLCLGLAERLRISPDVYINYYD MNAANVGWNN STFALEPKPSTPPGSSGCGAPGCCG

PMFIVNTNVP RASVPDGLSL ELTQQLAQAT GKPPQYIAVH VVPDQLMAFG GSSEPCALCS
LHSIGKIGGA QNRSYKLLCGLLAERLRISPRVYINYD MNAANVGWNN STFALEPKPSTPPGSSGGAPGGCG

5'CTGCCAGGGGCCCGGGTGCGGCGGTGGCCATCATCACCACCATCACCAGCGCTTCTCAGGAG-3'

RANKL-DOWN :

5'-CCGCTCGAGTTAGTCTATGTCTGAACITTTGAAAG-3'

318 and 319:

Protein sequence of GST-PS-C-RANKL (SEQ ID NO:318; capital letters)

cDNA sequence of GST-PS-C-RANKL (SEQ ID NO:319; small letters)

1 M S P I L G Y W K I K G L V Q P T R L L L E Y L E
 26 E K Y E E H L Y E R D E S D K W R N K K P E L G L
 76 g a a a a t a t g a a g a c a t t g t a t g a g c g c g a t g a a g t g a t a a t g c g a a c a a a a a g t t g a a t g g g t t g
 51 E P P N L P Y Y I D G D V K L T Q S M A I I R Y I
 151 g a g t t c c c a a t c t c t c t a t t a t a t g a t g g t g a t g t a a a t a a c a c a g t c t a t g c c a t c a t a c g t t a t a
 76 A D K H N M L G G C P K E R A E I S M L E G A V L
 226 g c t g a c a a g c a c a c a t g t t g g t g g t t g c c a a a g a g c g t g c a g a g a t t c a a t g c t t g a g g a g c g g t t g
 101 D I R Y G V S R I A Y S K D F E T L K V D F L S K
 301 g a t a t a g a t a c g t g t t c g a g a a t t g c a t a t a g t a a a g a c t t g a a a c t c t c a a a g t g a t t t c t t a g c a a g
 126 L P E M L K M F E D R L C H K T Y L N G D H V T H
 376 c t a c c t g a a a t g c t g a a a t g t t c g a a g a t c g t t a t g c a t a a a c a t a t t a a a t g g t g a t c a t g t a a c c a t
 151 P D F M L Y D A L D V V L Y M D P M C L D A F P K
 451 c e t g a c t c a t g t t g t a t g a c g t c t t g a t g t t g t t t a t a c a t g g a c c c a a t g t g c c t g g a t g c g t t c c c a a a a
 176 L V C P F K K R I E A I P Q I D K Y L K S S K Y I A
 526 t a g t t t g t t t a a a a a c g t a t t a g a c t a t c c c a a a a t t g a t a a g t a c t t g a a a t c c a a g a a t a t a t a g c a
 201 W P L Q G W Q A T F G G G D H P P K S D L E V L F
 601 t a g c c t t t g c a g g g c t g g c a a g c c a c g t t g g t g g t g g c g a c c a t c c t c a a a a t c g g a t c g g a a g t c t g t t c
 226 Q G P G C G G G G H H H H H Q R P S G A P A M V E
 676 c a g g g c c c g g g t g c g c g t g c c a t c a t a c c a c c a t c a c c a g c g c t t c t c a g g a g c t c c a g c a t a t a g c a a
 251 Q S H L D V A D Y G K P E A Q P A H L L I S A A
 751 G G C T C A T G G T T G A T G T G C C C A G C A G C A G C T G A G G C C C A G C C A T T T G C A C A C T C A C C A T C A A T G C T G C C
 276 S T P S G S R K V T I S S W T H D R G W A K I S N
 826 A G C A T C C C A T C G G G T T C C A T A A G T C A C T C T G C T C T T G G T A C C A G A T G A G G C T G G G C C A A G A T C T C T A A C
 301 M T L S N G K L R V N Q D G F Y Y L Y A N I C F R
 901 A T G A C G T T A G C A C G A A A C T A A G G T T A C A A G A T G G C T T C T A T A C T G T A G C C A C A T T T G C T T T G G
 326 H H T S C S V P D V L Q L V V V V K I S L
 976 C A T C A T G A A A C T C G G A A G C T A C T A C A G A C T A T C T C A G C T G A T G T G T A T G T G T A A A C C A G C A T C A A A
 351 I P S S H N L K Z G G S T K N W S G N S Z J H 7 Y
 1051 A T C C C A A G T T C T A T A A C C T G A T G A A A G G A G G A G C A G A A A A C T G G T C G G G C A A T C T G A A T C C A C T T T T A T
 376 S N V S G P P K L R A G P T S T C V S N P S I
 1126 T O C A T A A T G T T G G G G A T T T T C A A G C T C G A C T G T G A A G A A A T A G C A T C A G T G T C C A A C C C T T C C C T G
 401 L D P D Q D A Y P G A K K V Q D D
 1201 C T G A T C C G G A T C A A G T G C A G C A C T A C T T G G G G C T T T C A A A G T T C A G A C A T A G A C T A A C T G A G G G

1050393.01502

320:

Human-C-RANKL

GCGGGQHIRAEKAMVDGSLDLAKRSKLEAQPFAHLTINATDIPSGSHKVLSSWYHNRGAWAKISNMTFSNGKLI
 VNQDGFYYLIANICFRHHETSGDLATEYLLQMVYVTKTSIKIPSSHLMKGGSTKYWSNGSEFFHYFSINVGGF
 LRSGEISIEVSNPSLDDPDQDATYFGAFKVRDID

321:

Primer 5'PrP-BamHI

5'-CGG GAT CCC ACC ATG GTG GGG GGC CTT GG -3' (SEQ ID NO:321)

322:

Primer 3'PrP-NheI

5'-CTA GCT AGC CTG GAT CTT CTC CCG -3' (SEQ ID NO:322)

323:

Protein sequence of mPrP_E-E_K-Fc*

MVGGGLGGYMLGSAMSRPMIHFGNDWEDRYRENMYRYPNQVYYRPPVDQYSNQNNFVHDCVNTIKQHT
VTTTTKGENFTETDVKMMERVVEQMCVTQYQKESQAYYDGRSRLAGGGGCGDDDDKLTHTCPPCPAPEA
EGAPSVLFPFKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVS
VLTVLHQDWLNGKEYKCKVSNKALPASEIEKISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPS
DIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSSVMHEALHNHYTQKSLSLSPG
K

324:

mPrP_E

MVGGGLGGYMLGSAMSRPMIHFGNDWEDRYRENMYRYPNQVYYRPPVDQYSNQNNFVHDCVNTIKQHT
VTTTTKGENFTETDVKMMERVVEQMCVTQYQKESQAYYDGRSRLAGGGGCGDDDDK

325:

human resistin-C-Xa: (SEQ ID NO:325)

SSKTLCSMEEAINERIQEVAGSLIFRAISSIGLECQSVTSRGDL
ATCPRGFAVTGCTCGSACGSWDVRAETTCHCQCAGMDWTGARCCRVQPGGGGCG
IEGR

326:

human resistin-C-EK: (SEQ ID NO:326)

SSKTLCSMEEAINERIQEVAGSLIFRAISSIGLECQSVTSRGDL
ATCPRGFAVTGCTCGSACGSWDVRAETTCHCQCAGMDWTGARCCRVQPGGGGCG
DDDDK

327:

human resistin-C: (SEQ ID NO:327)

SSKTLCSMEEAINERIQEVAGSLIFRAISSIGLECQSVTSRGDL
ATCPRGFAVTGCTCGSACGSWDVRAETTCHCQCAGMDWTGARCCRVQPGGGGCG

328:

10050899.01302

ADPGCGGGGGLAIPTEIPTSALVKETLALLSTHRTLLIANETLRIPVPVHKNHQLCTEEIFQGIGTLESQTVQG
GTVERLFKNLSLIKKYIDGQKKKCGEERRRVNQFLDYLQEFLGVMNTEW IIES LEVLAIEGR

337:

human C-IL-5-S: (SEQ ID NO:337)

LACGGGGGIPTEIPTSALVKETLALLSTHRTLLIANETLRIPVPVHKNHQLCTEEIFQGIGTLESQTVQGGT
VERLFKNLSLIKKYIDGQKKKCGEERRRVNQFLDYLQEFLGVMNTEW IIES

338:

primer NheIL13-F: (SEQ ID NO:338)

CTAGCTAGCCGGGCCGGTGCCAAGATC

339:

primer XhoIL13-R: (SEQ ID NO:339)

TTTCTCGAGGAAGGGGCCGTGGCGAA

340:

primer Spelinker3-F1: (SEQ ID NO:340)

CCCCGCCGGGTCTTCTGGCGGTGCTCCGGCTAGCATGGAGATTCCCATGAGCAC

341:

Primer SpeNlinker3-F2: (SEQ ID NO:341)

TTTTACTAGTTGGTTGCGGCGGCCGAAACCGAGCACCCCGCCGGGTCTTC

342:

Primer IL5StopXho-R: (SEQ ID NO:342)

TTTTCGCGCCGCGTTTAAACTCGAGTTATTAGCCTTCCATTGCCCACTC

343:

Primer BamH1-FLK1-F: (SEQ ID NO:343)

CGCGGATCCATTCATCGCCTCTGTC

344:

Primer Nhe1-FLK1-B: (SEQ ID NO:344)

CTAGCTAGCTTTGTGTGAACTCGGAC

345:

mVEGFR-2 (2-3) fragment: (SEQ ID NO:345)

1050399.011802

PFIAS VSDQHGIYVI TENKNKTVVI PCRGSIISNLN VSLCARYPEK RFVPDGNRIS WDSEIGFTLP
SYMISYAGMV FCEAKINDET YQSIMYIVVV VGYRIYDVIL SPPHEIELSA GEKLVNLCTA
RTELNVGLDF TWHSPPSKSH HKKIVNRDVK PFPGTAKMF LSTLTIESVT KSDQGEYTCV
ASSGRMIKRN RTFVRVHTKP

346

human C-LT⁴⁹⁻³⁰⁶ : (SEQ ID NO:346)

LACGGQDQGRRVEKIIIGSAQAQKRLDDSKPSCILPSPSSLSETPDRLHPQRSNASRNLASTSQGPVAQSSR
EASAWMTILSPAADSTPDGVOQLPKGEPETDLNPELPAHLIGAWMSGQGLSWEASQEEAFLRSGAQFSP
THGLALPDQGVYYLYCHVGYRGRTTPAGRSRARSLLRSALYRAGGAYGRGSPPELLLEGAETVTPVVDPIG
YGSLWYTSVGFGLAQLRSGERVYVNISHPDMVDYRRGKTFFGAVMVG

347

human C-LT¹²⁶⁻³⁰⁶ : (SEQ ID NO:347)

LACGGSPAADSTPDGVOQLPKGEPETDLNPELPAHLIGAWMSGQGLSWEASQEEAFLRSGAQFSPHGL
ALPDQGVYYLYCHVGYRGRTTPAGRSRARSLLRSALYRAGGAYGRGSPPELLLEGAETVTPVVDPIGYGSL
WYTSVGFGLAQLRSGERVYVNISHPDMVDYRRGKTFFGAVMVG

348

Modified human prion protein fragment: (SEQ ID NO:348)

VGGLGGYMLGSAMSRPIIHFGSDYEDRYRENHRYPNQVYYRPMDE
YSNQNNFVHDCVNITKQHTVTTTCKGENFTETDVKMMERVVEQMCITQYERESQAYYQ
RGRLAGGGGCG

349

Modified bovine prion protein fragment: (SEQ ID NO:349)

VGGLGGYMLGSAMSRPLIHFGSDYEDRYRENHRYPNQVYYRVPDQ
YSNQNNFVHDCVNITVKHTVTTTCKGENFTETDIKMMERVVEQMCITQYQRESQAYYQ
RGRLAGGGGCG

350

Modified sheep prion protein fragment: (SEQ ID NO:350)

VGGLGGYMLGSAMSRPLIHFGNDYEDRYRENMYRYPNQVYYRVPDR
YSNQNNFVHDCVNITVKHTVTTTCKGENFTETDIKIMERVVEQMCITQYQRESQAYYQ
RGRLAGGGGCG

10050008.011002